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=> file biosis caba caplus embase japio lifesci medline scisearch
=> e kim bum joon/au
E1           48     KIM BUM JIN/AU
E2            1     KIM BUM JO/AU
E3          358 --> KIM BUM JOON/AU
E4            3     KIM BUM JOON DR/AU
E5            1     KIM BUM JOON DR PROF/AU
E6           43     KIM BUM JUN/AU
E7            1     KIM BUM JUNE/AU
E8            1     KIM BUM KEE/AU
E9            8     KIM BUM KEUN/AU
E10           5     KIM BUM KI/AU
E11           2     KIM BUM KWAN/AU
E12           4     KIM BUM KWON/AU
=> s e2-e7 and hsp?
L1           49 ("KIM BUM JO"/AU OR "KIM BUM JOON"/AU OR "KIM BUM JOON DR"/AU
                OR "KIM BUM JOON DR PROF"/AU OR "KIM BUM JUN"/AU OR "KIM BUM
                JUNE"/AU) AND HSP?
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           15 DUP REM L1 (34 DUPLICATES REMOVED)
=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y


L2   ANSWER 1 OF 15     MEDLINE on STN
AN   2009107816     MEDLINE <<LOGINID::20090617>>
DN   PubMed ID: 19041640
TI   Chicken Ovalbumin Upstream Promoter-Transcription Factor II (COUP-TFII)
     regulates growth and patterning of the postnatal mouse cerebellum.
AU     ***Kim Bum Jun***  ; Takamoto Norio; Yan Jun; Tsai Sophia Y; Tsai
     Ming-Jer
CS   Department of Molecular and Cellular Biology and Development Program,
     Baylor College of Medicine, Houston, TX 77030, USA.
NC   DK45641 (United States NIDDK NIH HHS)
     HD17379 (United States NICHD NIH HHS)
     HL076448 (United States NHLBI NIH HHS)
     P01 DK059820-060003 (United States NIDDK NIH HHS)
     P01 DK059820-070003 (United States NIDDK NIH HHS)
     P01 DK059820-080003 (United States NIDDK NIH HHS)
     P01DK59820 (United States NIDDK NIH HHS)
     R01 HD017379-22A1 (United States NICHD NIH HHS)
     R01 HD017379-23 (United States NICHD NIH HHS)
     R01 HD017379-24 (United States NICHD NIH HHS)
     R01 HL076448-02 (United States NHLBI NIH HHS)
     R01 HL076448-03 (United States NHLBI NIH HHS)
     R01 HL076448-04 (United States NHLBI NIH HHS)
     R37 DK045641-13 (United States NIDDK NIH HHS)
     R37 DK045641-14 (United States NIDDK NIH HHS)
     R37 DK045641-15 (United States NIDDK NIH HHS)
     R37 DK045641-16 (United States NIDDK NIH HHS)
     R37 DK045641-17 (United States NIDDK NIH HHS)
     U19 DK062434-010006 (United States NIDDK NIH HHS)
     U19 DK062434-01S10006 (United States NIDDK NIH HHS)
     U19 DK062434-01S19003 (United States NIDDK NIH HHS)
SO   Developmental biology, (2009 Feb 15) Vol. 326, No. 2, pp. 378-91.
     Electronic Publication: 2008-11-14.
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Journal code: 0372762. E-ISSN: 1095-564X.
Report No.: NLM-NIHMS94374; NLM-PMC2654226.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
LA English
FS Priority Journals
EM 200902
ED Entered STN: 3 Feb 2009
Last Updated on STN: 26 Feb 2009
Entered Medline: 25 Feb 2009
AB COUP-TFII (also known as Nr2f2), a member of the nuclear orphan receptor superfamily, is expressed in several regions of the central nervous system (CNS), including the ventral thalamus, hypothalamus, midbrain, pons, and spinal cord. To address the function of COUP-TFII in the CNS, we generated conditional COUP-TFII knockout mice using a tissue-specific NSE-Cre recombinase. Ablation of COUP-TFII in the brain resulted in malformation of the lobule VI in the cerebellum and a decrease in differentiation of cerebellar neurons and cerebellar growth. The decrease in cerebellar growth in NSE(Cre/+)/CII(F/F) mice is due to reduced proliferation and increased apoptosis in granule cell precursors (GCPs). Additional studies demonstrated that insulin like growth factor 1 (IGF-1) expression was reduced in the cerebellum of NSE(Cre/+)/CII(F/F) mice, thereby leading to decreased Akt1 and GSK-3beta activities, and the reduced expression of mTOR. Using ChIP assays, we demonstrated that COUP-TFII was recruited to the promoter region of IGF-1 in a Sp1-dependent manner. In addition, dendritic branching of Purkinje cells was decreased in the mutant mice. Thus, our results indicate that COUP-TFII regulates growth and maturation of the mouse postnatal cerebellum through modulation of IGF-1 expression.
AU ***Kim Bum Jun*** ; Takamoto Norio; Yan Jun; Tsai Sophia Y; Tsai Ming-Jer
CT . . . Proliferation
*Cerebellum: AH, anatomy & histology
*Cerebellum: GD, growth & development
Cerebellum: ME, metabolism
Glycogen Synthase Kinase 3: ME, metabolism
*** HSP70 Heat-Shock Proteins: ME, metabolism***
Humans
Insulin-Like Growth Factor I: GE, genetics
Insulin-Like Growth Factor I: ME, metabolism
Mice
Mice,. . .
CN 0 (COUP Transcription Factor II); 0 (Calcium-Binding Protein, Vitamin D-Dependent); 0 (Carrier Proteins); 0 (***HSP70*** Heat-Shock Proteins); 0 (RNA, Small Interfering); 0 (calbindin); 0 (calretinin); EC 2.7.1 (Frap1 protein, mouse); EC 2.7.1.- (Phosphotransferases (Alcohol Group. . .

L2 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
AN 2008:1298911 CAPLUS <<LOGINID::20090617>>
TI Proportions of Mycobacterium massiliense and Mycobacterium bolletii strains among Korean Mycobacterium chelonae-Mycobacterium abscessus group isolates
AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh
CS Department of Microbiology, Cancer Research Institute, Institute of

Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National University College of Medicine, Seoul National University Hospital, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2008), 46(10), 3384-3390
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English

AB Korean isolates of the Mycobacterium chelonae-Mycobacterium abscessus group, which had been isolated from two different hospitals in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the 144 rapidly growing mycobacterial strains tested, 127 strains (88.2%) belonged to the M. chelonae-M. abscessus group. In this group, M. chelonae, M. abscessus, M. massiliense, and M. bolletii accounted for 0.8% (n = 1), 51.2% (n = 65), 46.5% (n = 59), and 1.6% (n = 2), resp. Two isolates which showed discordant results, M. massiliense by rpoB sequence anal. and M. abscessus by ***hsp65*** sequence anal., were finally identified as M. massiliense based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. M. abscessus group I isolates previously identified by ***hsp65*** PRA were all found to be M. abscessus, whereas group II isolates were further identified as M. massiliense or M. bolletii by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh

AB . . . in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the. . . (n = 2), resp. Two isolates which showed discordant results, M. massiliense by rpoB sequence anal. and M. abscessus by ***hsp65*** sequence anal., were finally identified as M. massiliense based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. M. abscessus group I isolates previously identified by ***hsp65*** PRA were all found to be M. abscessus, whereas group II isolates were further identified as M. massiliense or M. bolletii by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were. . .

ST Mycobacterium ***hsp65*** rpoB 16S rRNA gene
IT INDEXING IN PROGRESS
IT INDEXING IN PROGRESS
IT Human
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense

(M. chelonae-M. abscessus group isolate from Korean patient show high prevalence of M. massiliense, M. abscessus and M. massiliense, M. bolletii accounted for M. abscessus group II strains identified by

hsp65 PCR restriction anal.)

L2 ANSWER 3 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
    DUPLICATE 2
AN 2008:322988 BIOSIS <<LOGINID::20090617>>
DN PREV200800322987
TI Mycobacterium senuense sp nov., a slowly growing, non-chromogenic species
    closely related to the Mycobacterium terrae complex.
AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
    Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst,
    Seoul 110799, South Korea
    kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (MAR
    2008) Vol. 58, No. Part 3, pp. 641-646.
    ISSN: 1466-5026.
DT Article
LA English
OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409;
    EMBL-DQ536409; DDJB-DQ536409
ED Entered STN: 29 May 2008
    Last Updated on STN: 29 May 2008
AB A previously undescribed, slowly growing, non-chromogenic mycobacterium,
    isolated from a Korean patient with a symptomatic pulmonary infection, is
    described as representing a novel species. Its 16S rRNA gene sequence was
    unique and phylogenetic analysis based on 16S rRNA gene sequences showed
    that this organism belonged to the Mycobacterium terrae subclade.
    Phenotypically, the strain was generally similar to M. terrae and
    Mycobacterium nonchromogenicum, but its growth rate was slower than those
    of other M. terrae complex strains. A unique mycolic acid profile and
    phylogenetic analysis based on two different alternative chronometer
    molecules, ***hsp65*** and rpoB, confirm the taxonomic status of this
    strain as a representative of a novel species. The name Mycobacterium
    senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM
    44999(T) =KCTC 19147(T)).
AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
    Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]
AB. . . other M. terrae complex strains. A unique mycolic acid profile and
    phylogenetic analysis based on two different alternative chronometer
    molecules, ***hsp65*** and rpoB, confirm the taxonomic status of this
    strain as a representative of a novel species. The name Mycobacterium
    senuense. . .
IT Major Concepts
       Population Genetics (Population Studies); Systematics and Taxonomy
IT Chemicals & Biochemicals
       rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]

L2 ANSWER 4 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
    DUPLICATE 3
AN 2008:636733 BIOSIS <<LOGINID::20090617>>
DN PREV200800636732
TI Differentiation of mycobacteria in sputa by duplex polymerase chain
    reaction for mycobacterial ***hsp65*** gene.
AU   ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae;
    Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick;
    Lee, Jae Seok; Yim, Jae-Joon
CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol,

Seoul 110744, South Korea
kbumjoon@snu.ac.kr; yimjj@snu.ac.kr
SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2, pp. 193-198.
CODEN: DMIDDZ. ISSN: 0732-8893.
DT Article
LA English
ED Entered STN: 19 Nov 2008
Last Updated on STN: 19 Nov 2008
AB Early differentiation of mycobacteria in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. Mycobacterial species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of mycobacterial species were made based on 1) results of species identification based on mycobacterial colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous mycobacteria patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for Mycobacterium tuberculosis were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate mycobacterial species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.
TI Differentiation of mycobacteria in sputa by duplex polymerase chain reaction for mycobacterial ***hsp65*** gene.
AU ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae. . .
AB. . . is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. Mycobacterial species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the
conventional colony-based method. Final decision of mycobacterial species were made. . .
GEN Mycobacterium ***hsp65*** gene (Mycobacteriaceae)

L2 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:1057364 CAPLUS <<LOGINID::20090617>>
DN 147:337125
TI Method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence
IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon
PA Seoul National University Industry Foundation, S. Korea
SO Repub. Korea, No pp. given
CODEN: KRXXFC

DT Patent
LA Korean
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		

AB A method for identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria is provided to conveniently and accurately differentiate Mycobacterial species by using each 8 signature nucleotide sequences capable of characterizing Mycobacterium tuberculosis group and non-tuberculous mycobacteria group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of Mycobacterial species using a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to identify non-tuberculous mycobacteria and Mycobacterium tuberculosis, where the non-tuberculous mycobacteria is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the Mycobacterium tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of primer pair for producing PCR amplification product specific to the non-tuberculous mycobacteria is described. The differentiation kit for non-tuberculous mycobacteria and Mycobacterium tuberculosis comprises a primer pairs, and the sequences of the primers have been presented.

TI Method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence

IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon

AB . . . consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of Mycobacterial species using a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the. . .

ST Mycobacterium tuberculosis nontuberculous genotyping PCR ***Hsp65*** gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 65; method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

IT Genotypes
Genotyping (method)
Mycobacterium
Mycobacterium tuberculosis
Polymerase chain reaction
Tuberculosis
(method for differentiating or identifying Mycobacterium tuberculosis

and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

L2 ANSWER 6 OF 15 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:1225201 SCISEARCH <<LOGINID::20090617>>
GA The Genuine Article (R) Number: 231FU
TI Case of pyomyositis due to Mycobacterium haemophilum in a renal transplant recipient
AU Choi, Sang-Ho (Reprint)
CS Univ Ulsan, Coll Med, Asan Med Ctr, Div Infect Dis, Seoul 138736, South Korea (Reprint)
AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na; ***Kim, Bum-Joon*** ; Kim, Yang Soo; Woo, Jun Hee
CS Univ Ulsan, Coll Med, Asan Med Ctr, Dept Lab Med, Seoul 138736, South Korea; Seoul Natl Univ, Coll Med, Liver Res Inst, Canc Res Inst, Dept Microbiol & Immunol, Seoul, South Korea
E-mail: sangho@amc.seoul.kr
CYA South Korea
SO JOURNAL OF CLINICAL MICROBIOLOGY, (NOV 2007) Vol. 45, No. 11, pp. 3847-3849.
ISSN: 0095-1137.
PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DT Article; Journal
LA English
REC Reference Count: 13
ED Entered STN: 13 Dec 2007
Last Updated on STN: 13 Dec 2007
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We report a case of pyomyositis due to Mycobacterium haemophilum in a renal transplant recipient. M. haemophilum was identified by PCR-mediated sequence analysis of the heat shock protein gene in the DNA of the specimen. The patient was successfully treated with repeated surgical debridement and prolonged anti-mycobacterial therapy.
AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na; ***Kim, Bum-Joon*** ; Kim, Yang Soo; Woo, Jun Hee
STP KeyWords Plus (R): GENE ***HSP65*** ; IDENTIFICATION; PATIENT; RPOB; AVIUM; AIDS

L2 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4
AN 2007:1135732 CAPLUS <<LOGINID::20090617>>
DN 148:281748
TI Outbreak of Mycobacterium massiliense infection associated with intramuscular injections
AU Kim, Hee-Youn; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh
CS Department of Microbiology, Cancer Research Institute, Institute of Endemic Diseases, SNUMRC, S. Korea
SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
DT Journal
LA English
AB Twelve strains of a rapidly growing Mycobacterium species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as Mycobacterium massiliense (100% similarity).
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AU . . . Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; ***Kim,*** ***Bum-Joon*** ; Kook, Yoon-Hoh
AB . . . an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as Mycobacterium massiliense (100% similarity).
ST Mycobacterium infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65*** Mycobacterium infection taxonomy epidemiol
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** 65, gene ***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)
IT Evolution
(mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

L2 ANSWER 8 OF 15 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:1211730 SCISEARCH <<LOGINID::20090617>>
GA The Genuine Article (R) Number: 228MD
TI Pulmonary disease caused by Mycobacterium xenopi: The first case in Korea
AU Koh, Won-Jung (Reprint)
CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, 50 Irwan Dong, Seoul, South Korea (Reprint)
AU Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***
CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Lab Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Thorac Surg, Seoul, South Korea; Korean Natl TB Assoc, Korean Inst TB, Seoul, South Korea; Seoul Natl Univ, Coll Med, Dept Microbiol & Immunol, Seoul, South Korea; Seoul Natl Univ, Coll Med, Canc Res Inst, Seoul, South Korea
E-mail: wjkoh@skku.edu
CYA South Korea
SO YONSEI MEDICAL JOURNAL, (31 OCT 2007) Vol. 48, No. 5, pp. 871-875. ISSN: 0513-5796.
PB YONSEI UNIV COLLEGE MEDICINE, C/O KYUN0-IL IM, M.D., PH.D, SHINCHON DONG 134, SEODAEMOON KU, SEOUL 120-752, SOUTH KOREA.

DT Article; Journal
LA English
REC Reference Count: 20
ED Entered STN: 6 Dec 2007
Last Updated on STN: 6 Dec 2007
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Mycobacterium xenopi is a nontuberculous mycobacterium (NTM) that rarely causes pulmonary disease in Asia. Here we describe the first case of M xenopi pulmonary disease in Korea. A 66-year-old man was admitted to our hospital with a 2-month history of productive cough and hemoptysis. His past medical history included pulmonary tuberculosis 44 years earlier, leading to a right upper lobectomy. Chest X-ray upon admission revealed cavitary consolidation involving the entire right lung. Numerous acid-fast bacilli were seen in his initial sputum, and M xenopi was subsequently identified in more than five sputum cultures, using molecular methods. Despite treatment with clarithromycin, rifampicin, ethambutol, and streptomycin, the infiltrative shadow revealed on chest X-ray increased in size. The patient's condition worsened, and a right completion pneumonectomy was performed. The patient consequently died of respiratory failure on postoperative day 47, secondary to the development of a late bronchopleural fistula. This case serves as a reminder to clinicians that the incidence of NTM infection is increasing in Korea and that unusual NTM are capable of causing disease in non-immunocompromised patients.
AU. . . Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***
STP KeyWords Plus (R): NONTUBERCULOUS MYCOBACTERIA; INFECTION; DIFFERENTIATION; CLARITHROMYCIN; SPECIMENS; PATIENT; ***HSP65*** ; GENE

L2 ANSWER 9 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 5
AN 2007:338789 BIOSIS <<LOGINID::20090617>>
DN PREV200700342042
TI Mycobacterium seoulense sp nov., a slowly growing scotochromogenic species.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2007) Vol. 57, No. Part 3, pp. 594-599.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 6 Jun 2007
Last Updated on STN: 6 Jun 2007
AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its

unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** *** Bum-Joon*** [Reprint Author]

AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and. . . M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that. . .

GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium rpoB gene (Mycobacteriaceae): expression

L2 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2007:465634 CAPLUS <<LOGINID::20090617>>

DN 147:339410

TI Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** *** Bum-Joon***

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO International Journal of Systematic and Evolutionary Microbiology (2007), 57(3), 593-599
CODEN: ISEMF5; ISSN: 1466-5026

PB Society for General Microbiology

DT Journal

LA English

AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon***

AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and. . . M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that. . .

ST Mycobacterium scotochromogenic 16S rRNA gene rpoB ***hsp65*** sequence

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** 65; Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***hsp65*** ; Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species)

L2 ANSWER 11 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6

AN 2007:135186 BIOSIS <<LOGINID::20090617>>

DN PREV200700134974

TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
CODEN: MIIMDV. ISSN: 0385-5600.

DT Article

LA English

ED Entered STN: 22 Feb 2007
Last Updated on STN: 22 Feb 2007

AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic mycobacteria from clinical specimens, we applied this method to 40 sputum samples and compared the results to those obtained by IS6110 PCR. Although this method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs. 100%), it detected infections of M. avium complex (MAC) in two patients, which was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic mycobacteria in primary clinical specimens.

TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai,

Gil-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]

AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic mycobacteria from clinical specimens, we applied this method to 40 sputum samples and. . .

GEN Mycobacterium avium ***hsp65*** gene [Mycobacterium avium heat shock protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium tuberculosis ***hsp65*** gene [Mycobacterium tuberculosis heat shock protein 65 gene] (Mycobacteriaceae): expression

L2 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7

AN 2006:1304935 CAPLUS <<LOGINID::20090617>>

DN 146:515458

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon***

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying mycobacterial culture isolates at the species level.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon***

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin.. . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . .

ST Mycobacterium species differentiation ***hsp65*** duplex PCR

restriction analysis sequencing
IT DNA sequence analysis
Mycobacterium tuberculosis
Tuberculosis
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Genetic methods
(duplex-PCR-based restriction anal.; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Polymerase chain reaction
(duplex; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Human
(isolates from; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Diagnosis
(mol.; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Mycobacterium
(nontuberculosis; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
936858-61-6 936858-62-7 936858-64-9 936858-65-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

L2 ANSWER 13 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 8
AN 2005:448449 BIOSIS <<LOGINID::20090617>>
DN PREV200510237956
TI Differentiation of Mycobacterium species by analysis of the heat-shock protein 65 gene (***hsp65***).
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (JUL 2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005
AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 Mycobacterium strains containing 56 reference Mycobacterium species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between Mycobacterium species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus
revealing natural relationships among Mycobacterium species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous mycobacterium (NTM) clinical isolates, all NTMs were clearly identified. In addition, an XhoI PCR restriction fragment length polymorphism analysis method for the differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.
TI Differentiation of Mycobacterium species by analysis of the heat-shock protein 65 gene (***hsp65***).
AU. . . Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]
AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 Mycobacterium strains containing 56 reference Mycobacterium species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between Mycobacterium species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus
revealing natural relationships among Mycobacterium species. When a. . . differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.
IT . . .
Genetics (Population Studies); Systematics and Taxonomy
IT Chemicals & Biochemicals
16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [***HSP65***]
GEN Mycobacterium 16S rRNA gene (Mycobacteriaceae); Mycobacterium ***hsp65*** gene [Mycobacterium heat-shock protein 65 gene gene] (Mycobacteriaceae)

L2 ANSWER 14 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9
AN 2005:437869 BIOSIS <<LOGINID::20090617>>

DN PREV200510224308
TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
CODEN: JMIMDQ. ISSN: 0167-7012.
DT Article
LA English
ED Entered STN: 26 Oct 2005
Last Updated on STN: 26 Oct 2005
AB A method based on PCR-restiiction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the mycobacteria species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of M avium, M intracellulare and M tuberculosis to the species level by AvaII digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of mycobacteria culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.
TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,*** ***Bum-Joon*** [Reprint Author]
AB A method based on PCR-restiiction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with. . .
GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae)

L2 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:591378 CAPLUS <<LOGINID::20090617>>
DN 139:146183
TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species
IN ***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi
PA Biomedlab Corporation, S. Korea
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species

IN ***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi

AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .

ST primer mycobacteria heat shock protein ***hsp65*** gene

IT Nucleic acid amplification (method)
(DNA; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT Diagnosis
(mol.; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium
Mycobacterium avium paratuberculosis
Mycobacterium bovis
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium leprae
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium microti
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium parafortuitum
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium simiae
Mycobacterium smegmatis
Mycobacterium szulgai
Mycobacterium terrae
Mycobacterium thermoresistibile
Mycobacterium triviale
Mycobacterium tuberculosis
Mycobacterium ulcerans
Mycobacterium vaccae
Mycobacterium wolinskyi
Nocardia carnea

RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
569432-52-6 569432-53-7 569432-54-8 569432-55-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-56-0
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPF3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-57-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPR3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569477-29-8
RL: PRP (Properties)
(unclaimed sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

=> e kook yoon ho/au
E1 3 KOOK YOON BUM/AU

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E2            1     KOOK YOON HAWN/AU
E3            4 --> KOOK YOON HO/AU
E4          288     KOOK YOON HOH/AU
E5            1     KOOK YOON HOH DR/AU
E6            1     KOOK YOON HOH*/AU
E7           10     KOOK YOON HWAN/AU
E8            3     KOOK YOON SANG/AU
E9            1     KOOK YOONAH/AU
E10           1     KOOK YOONBUM/AU
E11           1     KOOK YOONHO/AU
E12          14     KOOK YOONHOH/AU

=> s e3-e6 and hsp?
L3           45 ("KOOK YOON HO"/AU OR "KOOK YOON HOH"/AU OR "KOOK YOON HOH DR"/A
                U OR "KOOK YOON HOH*"/AU) AND HSP?

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            11 DUP REM L3 (34 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 11 ANSWERS - CONTINUE? Y/(N):y


L4   ANSWER 1 OF 11  CAPLUS  COPYRIGHT 2009 ACS on STN DUPLICATE 1
AN   2008:1298911  CAPLUS <<LOGINID::20090617>>
TI   Proportions of Mycobacterium massiliense and Mycobacterium bolletii
     strains among Korean Mycobacterium chelonae-Mycobacterium abscessus group
     isolates
AU   Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam
     Yong; Shim, Tae Sun; Kim, Bum-Joon;   ***Kook, Yoon-Hoh***
CS   Department of Microbiology, Cancer Research Institute, Institute of
     Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National
     University College of Medicine, Seoul National University Hospital, Seoul,
     110-799, S. Korea
SO   Journal of Clinical Microbiology (2008), 46(10), 3384-3390
     CODEN: JCMIDW; ISSN: 0095-1137
PB   American Society for Microbiology
DT   Journal
LA   English
AB   Korean isolates of the Mycobacterium chelonae-Mycobacterium abscessus
     group, which had been isolated from two different hospitals in South
     Korea, were identified by PCR restriction anal. (PRA) and comparative
     sequence anal. of 16S rRNA genes, rpoB, and   ***hsp65***   to evaluate
     the proportion of four closely related species (M. chelonae, M. abscessus,
     M. massiliense, and M. bolletii).  Of the 144 rapidly growing
     mycobacterial strains tested, 127 strains (88.2%) belonged to the M.
     chelonae-M. abscessus group.  In this group, M. chelonae, M. abscessus, M.
     massiliense, and M. bolletii accounted for 0.8% (n = 1), 51.2% (n = 65),
     46.5% (n = 59), and 1.6% (n = 2), resp.  Two isolates which showed
     discordant results, M. massiliense by rpoB sequence anal. and M. abscessus
     by   ***hsp65***   sequence anal., were finally identified as M.
     massiliense based on the addnl. anal. of sodA and the 16S-23S internal
     transcribed spacer.  M. abscessus group I isolates previously identified
     by   ***hsp65***   PRA were all found to be M. abscessus, whereas group II
     isolates were further identified as M. massiliense or M. bolletii by
     sequencing of rpoB and   ***hsp65***  .  Smooth, rough, or mixed colonies
```

of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

AB . . . in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (M. chelonae, M. abscessus, M. massiliense, and M. bolletii). Of the. . . (n = 2), resp. Two isolates which showed discordant results, M. massiliense by rpoB sequence anal. and M. abscessus by ***hsp65*** sequence anal., were finally identified as M. massiliense based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. M. abscessus group I isolates previously identified by ***hsp65*** PRA were all found to be M. abscessus, whereas group II isolates were further identified as M. massiliense or M. bolletii by sequencing of rpoB and ***hsp65*** . Smooth, rough, or mixed colonies of both M. abscessus and M. massiliense isolates were obsd. M. massiliense strains that were. . .

ST Mycobacterium ***hsp65*** rpoB 16S rRNA gene

IT INDEXING IN PROGRESS

IT INDEXING IN PROGRESS

IT Human
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense
(M. chelonae-M. abscessus group isolate from Korean patient show high prevalence of M. massiliense, M. abscessus and M. massiliense, M. bolletii accounted for M. abscessus group II strains identified by ***hsp65*** PCR restriction anal.)

L4 ANSWER 2 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2

AN 2008:322988 BIOSIS <<LOGINID::20090617>>

DN PREV200800322987

TI Mycobacterium senuense sp nov., a slowly growing, non-chromogenic species closely related to the Mycobacterium terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2008) Vol. 58, No. Part 3, pp. 641-646.
ISSN: 1466-5026.

DT Article

LA English

OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409; EMBL-DQ536409; DDJB-DQ536409

ED Entered STN: 29 May 2008
Last Updated on STN: 29 May 2008

AB A previously undescribed, slowly growing, non-chromogenic mycobacterium, isolated from a Korean patient with a symptomatic pulmonary infection, is described as representing a novel species. Its 16S rRNA gene sequence was

unique and phylogenetic analysis based on 16S rRNA gene sequences showed that this organism belonged to the Mycobacterium terrae subclade. Phenotypically, the strain was generally similar to M. terrae and Mycobacterium nonchromogenicum, but its growth rate was slower than those of other M. terrae complex strains. A unique mycolic acid profile and phylogenetic analysis based on two different alternative chronometer molecules, ***hsp65*** and rpoB, confirm the taxonomic status of this strain as a representative of a novel species. The name Mycobacterium senuense sp. nov. is proposed, with the type strain 05-832(T) (=DSM 44999(T) =KCTC 19147(T)).

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB. . . other M. terrae complex strains. A unique mycolic acid profile and phylogenetic analysis based on two different alternative chronometer molecules, ***hsp65*** and rpoB, confirm the taxonomic status of this strain as a representative of a novel species. The name Mycobacterium senuense. . .

IT Major Concepts
Population Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals
rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]

L4 ANSWER 3 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 3

AN 2008:636733 BIOSIS <<LOGINID::20090617>>

DN PREV200800636732

TI Differentiation of mycobacteria in sputa by duplex polymerase chain reaction for mycobacterial ***hsp65*** gene.

AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon

CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol, Seoul 110744, South Korea
kbumjoon@snu.ac.kr; yimjj@snu.ac.kr

SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2, pp. 193-198.
CODEN: DMIDDZ. ISSN: 0732-8893.

DT Article

LA English

ED Entered STN: 19 Nov 2008
Last Updated on STN: 19 Nov 2008

AB Early differentiation of mycobacteria in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. Mycobacterial species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of mycobacterial species were made based on 1) results of species identification based on mycobacterial colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous mycobacteria patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for Mycobacterium tuberculosis

were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate mycobacterial species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

TI Differentiation of mycobacteria in sputa by duplex polymerase chain reaction for mycobacterial ***hsp65*** gene.

AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon

AB. . . is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. Mycobacterial species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of mycobacterial species were made. . .

GEN Mycobacterium ***hsp65*** gene (Mycobacteriaceae)

L4 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4

AN 2007:1135732 CAPLUS <<LOGINID::20090617>>

DN 148:281748

TI Outbreak of Mycobacterium massiliense infection associated with intramuscular injections

AU Kim, Hee-Youn; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

CS Department of Microbiology, Cancer Research Institute, Institute of Endemic Diseases, SNUMRC, S. Korea

SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Twelve strains of a rapidly growing Mycobacterium species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as Mycobacterium massiliense (100% similarity).

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU . . . Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook,*** ***Yoon-Hoh***

AB . . . an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65*** . These isolates were identified as Mycobacterium massiliense (100% similarity).

ST Mycobacterium infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65*** Mycobacterium infection taxonomy epidemiol

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***HSP*** 65, gene ***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Evolution
(mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

L4 ANSWER 5 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 5
AN 2007:338789 BIOSIS <<LOGINID::20090617>>
DN PREV200700342042
TI Mycobacterium seoulense sp nov., a slowly growing scotochromogenic species.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2007) Vol. 57, No. Part 3, pp. 594-599.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 6 Jun 2007
Last Updated on STN: 6 Jun 2007
AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and. . . M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a

novel species. These data support the conclusion that. . .
GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium rpoB gene (Mycobacteriaceae): expression

L4 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:465634 CAPLUS <<LOGINID::20090617>>
DN 147:339410
TI Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon
CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea
SO International Journal of Systematic and Evolutionary Microbiology (2007), 57(3), 593-599
CODEN: ISEMF5; ISSN: 1466-5026
PB Society for General Microbiology
DT Journal
LA English
AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon
AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and. . . M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that. . .
ST Mycobacterium scotochromogenic 16S rRNA gene rpoB ***hsp65*** sequence
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***HSP*** 65; Mycobacterium seoulense sp. nov., a slowly growing

scotochromogenic species)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***hsp65*** ; Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species)

L4 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6
AN 2007:135186 BIOSIS <<LOGINID::20090617>>
DN PREV200700134974
TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
CODEN: MIIMDV. ISSN: 0385-5600.
DT Article
LA English
ED Entered STN: 22 Feb 2007
Last Updated on STN: 22 Feb 2007
AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic mycobacteria from clinical specimens, we applied this method to 40 sputum samples and compared the results to those obtained by IS6110 PCR. Although this method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs. 100%), it detected infections of M. avium complex (MAC) in two patients, which was not possible by IS6110 PCR. We conclude that Avall PRA is a highly effective method for directly detecting pathogenic mycobacteria in primary clinical specimens.
TI Direct application of AvaII PCR restriction fragment length polymorphism analysis (AvaII PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.
AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
AB To evaluate the usefulness of the AvaII PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic mycobacteria from clinical specimens, we applied this method to 40 sputum samples and. . .
GEN Mycobacterium avium ***hsp65*** gene [Mycobacterium avium heat shock protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium tuberculosis ***hsp65*** gene [Mycobacterium tuberculosis heat shock protein 65 gene] (Mycobacteriaceae): expression

L4 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7
AN 2006:1304935 CAPLUS <<LOGINID::20090617>>
DN 146:515458
TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing
AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim,

Bum-Joon

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying mycobacterial culture isolates at the species level.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin.. . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . .

ST Mycobacterium species differentiation ***hsp65*** duplex PCR restriction analysis sequencing

IT DNA sequence analysis
Mycobacterium tuberculosis
Tuberculosis
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Genetic methods
(duplex-PCR-based restriction anal.; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Polymerase chain reaction
(duplex; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct

sequencing)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Human
(isolates from; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Diagnosis
(mol.; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Mycobacterium
(nontuberculosis; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5 936858-61-6 936858-62-7 936858-64-9 936858-65-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

L4 ANSWER 9 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 8
AN 2005:448449 BIOSIS <<LOGINID::20090617>>
DN PREV200510237956
TI Differentiation of Mycobacterium species by analysis of the heat-shock protein 65 gene (***hsp65***).
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,*** *** Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (JUL 2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005
AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 Mycobacterium strains containing 56 reference Mycobacterium species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between Mycobacterium species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus

revealing natural relationships among Mycobacterium species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous mycobacterium (NTM) clinical isolates, all NTMs were clearly identified. In addition, an XhoI PCR restriction fragment length polymorphism analysis method for the differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.

TI Differentiation of Mycobacterium species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,*** ***Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 Mycobacterium strains containing 56 reference Mycobacterium species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between Mycobacterium species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene, thus revealing natural relationships among Mycobacterium species. When a. . . differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.

IT . . .
Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals
16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [***HSP65***]

GEN Mycobacterium 16S rRNA gene (Mycobacteriaceae); Mycobacterium ***hsp65*** gene [Mycobacterium heat-shock protein 65 gene gene] (Mycobacteriaceae)

L4 ANSWER 10 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9

AN 2005:437869 BIOSIS <<LOGINID::20090617>>

DN PREV200510224308

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
CODEN: JMIMDQ. ISSN: 0167-7012.

DT Article

LA English

ED Entered STN: 26 Oct 2005
Last Updated on STN: 26 Oct 2005

AB A method based on PCR-restiiction fragment length polymorphism analysis

(PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the mycobacteria species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of M avium, M intracellulare and M tuberculosis to the species level by AvaII digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of mycobacteria culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB A method based on PCR-restiiction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with. . .

GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae)

L4 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2003:591378 CAPLUS <<LOGINID::20090617>>

DN 139:146183

TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species

IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi

PA Biomedlab Corporation, S. Korea

SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003062470	A1	20030731	WO 2003-KR131	20030121
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
KR 2003063935	A	20030731	KR 2002-4297	20020124
KR 2003072087	A	20030913	KR 2002-11648	20020305

PI US 20050014157 A1 20050120 US 2004-500586 20040909
PRAI KR 2002-4297 A 20020124
KR 2002-11648 A 20020305
WO 2003-KR131 W 20030121
AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species
IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi
AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .
ST primer mycobacteria heat shock protein ***hsp65*** gene
IT Nucleic acid amplification (method)
(DNA; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT Diagnosis
(mol.; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)
IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium

Mycobacterium avium paratuberculosis
Mycobacterium bovis
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium leprae
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium microti
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium parafortuitum
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium simiae
Mycobacterium smegmatis
Mycobacterium szulgai
Mycobacterium terrae
Mycobacterium thermoresistibile
Mycobacterium triviale
Mycobacterium tuberculosis
Mycobacterium ulcerans
Mycobacterium vaccae
Mycobacterium wolinskyi
Nocardia carnea
RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1

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     569432-32-2   569432-33-3   569432-34-4   569432-35-5   569432-36-6
     569432-37-7   569432-38-8   569432-39-9   569432-40-2   569432-41-3
     569432-42-4   569432-43-5   569432-44-6   569432-45-7   569432-46-8
     569432-47-9   569432-48-0   569432-49-1   569432-50-4   569432-51-5
     569432-52-6   569432-53-7   569432-54-8   569432-55-9
     RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
     DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
     (Biological study); USES (Uses)
        (nucleotide sequence; primers for amplifying mycobacterial heat shock
        protein   ***HSP***   65 gene and use for identifying mycobacterial
        species)
IT   569432-56-0
     RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
     DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
     (Biological study); USES (Uses)
        (primer   ***HSPF3***   sequence; primers for amplifying mycobacterial
        heat shock protein   ***HSP***   65 gene and use for identifying
        mycobacterial species)
IT   569432-57-1
     RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
     DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
     (Biological study); USES (Uses)
        (primer   ***HSPR3***   sequence; primers for amplifying mycobacterial
        heat shock protein   ***HSP***   65 gene and use for identifying
        mycobacterial species)
IT   81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (primers for amplifying mycobacterial heat shock protein   ***HSP***
        65 gene and use for identifying mycobacterial species)
IT   569477-29-8
     RL: PRP (Properties)
        (unclaimed sequence; primers for amplifying mycobacterial heat shock
        protein   ***HSP***   65 gene and use for identifying mycobacterial
        species)


=> e kim jeong mi/au
E1           1     KIM JEONG MANN/AU
E2          30     KIM JEONG MEE/AU
E3         150 --> KIM JEONG MI/AU
E4         464     KIM JEONG MIN/AU
E5           2     KIM JEONG MM/AU
E6          15     KIM JEONG MO/AU
E7           4     KIM JEONG MOG/AU
E8          39     KIM JEONG MOK/AU
E9           1     KIM JEONG MONG/AU
E10         16     KIM JEONG MOOG/AU
E11          5     KIM JEONG MOOK/AU
E12          3     KIM JEONG MOON/AU

=> s e2-e4 and hsp?
L5          33 ("KIM JEONG MEE"/AU OR "KIM JEONG MI"/AU OR "KIM JEONG MIN"/AU)
               AND HSP?

=> dup rem l5
PROCESSING COMPLETED FOR L5
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L6 5 DUP REM L5 (28 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 5 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:42683 CAPLUS <<LOGINID::20090617>>
DN 148:71211
TI Epilepsy diagnostic kit for diagnosing epilepsy via expression degree of epilepsy marker genes
IN Kim, Nam Sun; Jung, So Yeong; Wang, Ae Guk; Oh, Jeong Hwa; Byun, Sang Sun; ***Kim, Jeong Min*** ; Lee, Dong Seok; Jung, Cheon Gi; Lee, Yun Jin
PA Korea Research Institute of Bioscience and Biotechnology, S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, 29pp.
CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 2007116555	A	20071210	KR 2007-54409	20070604
	KR 900764	B1	20090602		
PRAI	KR 2006-50227	A	20060605		

AB The title epilepsy diagnostic kit can diagnose epilepsy via expression degree of epilepsy marker genes, including GAPDH, TSC22, TTR, DEPP, SPP1, ACTG2, ID2, HNLF, CPE, MBP, LDHA, ***HSPA9B*** , A2BP1, PPP2CA, ATP6VE1, MAP2, MGC8685, HLA-C, ARF1 and VSNL1. The epilepsy diagnostic kit contains: (1) the above genes, (2) probes of 200bp complementary to the above genes, and (3) more than one of sense primers and sequences of antisense primers of the above genes.
IN Kim, Nam Sun; Jung, So Yeong; Wang, Ae Guk; Oh, Jeong Hwa; Byun, Sang Sun; ***Kim, Jeong Min*** ; Lee, Dong Seok; Jung, Cheon Gi; Lee, Yun Jin
AB . . . epilepsy via expression degree of epilepsy marker genes, including GAPDH, TSC22, TTR, DEPP, SPP1, ACTG2, ID2, HNLF, CPE, MBP, LDHA, ***HSPA9B*** , A2BP1, PPP2CA, ATP6VE1, MAP2, MGC8685, HLA-C, ARF1 and VSNL1. The epilepsy diagnostic kit contains: (1) the above genes, (2) probes. . .
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(***HSPA9B*** ; epilepsy diagnostic kit for diagnosing epilepsy via expression degree of epilepsy marker genes)

L6 ANSWER 2 OF 5 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 1
AN 2007:363762 BIOSIS <<LOGINID::20090617>>
DN PREV200700362958
TI Valproic acid-mediated neuroprotection in intracerebral hemorrhage via histone deacetylase inhibition and transcriptional activation.
AU Sinn, Dong-In; Kim, Se-Jeong; Chu, Kon; Jung, Keun-Hwa; Lee, Soon-Tae; Song, Eun-Cheol; ***Kim, Jeong-Min*** ; Park, Dong-Kyu; Lee, Sang Kun; Kim, Manho; Roh, Jae-Kyu [Reprint Author]
CS Seoul Natl Univ Hosp, Dept Neurol,SNUMRC, Stroke and Neural Stem Cell Lab,Neurosci Res Inst, Clin Res Inst,Stem Cell Res Ctr, 28,Yongon Dong, Seoul 110744, South Korea
rohjk@snu.ac.kr

SO Neurobiology of Disease, (MAY 2007) Vol. 26, No. 2, pp. 464-472.
ISSN: 0969-9961.
DT Article
LA English
ED Entered STN: 20 Jun 2007
Last Updated on STN: 20 Jun 2007
AB The modification of histone N-terminal tails by acetylation or deacetylation can alter the interaction between histories and DNA, and thus regulate gene expression. Recent experiments have demonstrated that valproic acid (VPA), a well-known anti-epileptic drug, can directly inhibit histone deacetylase (HDAC) activity and cause the by hyperacetylation of histones. Moreover, VIA has been shown to mediate neuronal protection by activating signal transduction pathways and by inhibiting proapoptotic factors. In this study, we attempted to determine whether VPA alleviates cerebral inflammation and perihematomal cell death after intracerebral hemorrhage (ICH). Adult male rats received intraperitoneal injections of 300 mg/kg VIA or PBS twice a day after ICH induction. VPA treatment inhibited hematoma expansion, perihematomal cell death, caspase activities, and inflammatory cell infiltration. In addition, VPA treatment had the following expressional effects; it activated the translations of acetylated histone H3, pERK, pAKT, pCREB, and ***HSP70*** ; up-regulated bcl-2 and bcl-xl but down-regulated bax; and down-regulated the mRNAs of Fas-L, IL-6, MMP-9, MIP-1, MCP-J, and tPA. VPA-treated rats also showed better functional recovery from I day to 4 weeks after ICH. Here we show that VPA induces neuroprotection in a murine ICH model and that its neuroprotective effects are mediated by transcriptional activation following HDAC inhibition. (c) 2007 Elsevier Inc. All rights reserved.
AU Sinn, Dong-In; Kim, Se-Jeong; Chu, Kon; Jung, Keun-Hwa; Lee, Soon-Tae; Song, Eun-Cheol; ***Kim, Jeong-Min*** ; Park, Dong-Kyu; Lee, Sang Kun; Kim, Manho; Roh, Jae-Kyu [Reprint Author]
AB. . . addition, VPA treatment had the following expressional effects; it activated the translations of acetylated histone H3, pERK, pAKT, pCREB, and ***HSP70*** ; up-regulated bcl-2 and bcl-xl but down-regulated bax; and down-regulated the mRNAs of Fas-L, IL-6, MMP-9, MIP-1, MCP-J, and tPA. VPA-treated. . .
IT . . .
intracerebral hemorrhage: vascular disease, nervous system disease, drug therapy
Cerebral Hemorrhage (MeSH)
IT Chemicals & Biochemicals
DNA; IL-6 [interleukin-6]; bcl-2; MCP-1; ***HSP70*** [heat shock protein 70]; H3 histone; caspase [EC 3.4.22.36]: inhibition; tPA; bax; pERK; bcl-xl; pCREB; MMP-9 [EC 3.4.24.35]; pAKT; MIP-1;. . .

L6 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:14598 CAPLUS <<LOGINID::20090617>>
DN 142:111833
TI Expressed sequence tags identifying marker genes for the diagnosis of gastric cancer and metastatic gastric cancer
IN Kim, Nam-Soon; Kim, Yong Sung; Lee, Ju-Yeon; Oh, Jung-Hwa; Park, Hong-Seog; Ahn, Hee-Young; Yoon, Sun-Young; Han, Yoonsoo; Kim, Sangsoo; ***Kim, Jeong-Min*** ; Byun, Sang-Soon; Noh, Seung-Moo; Song, Kyu-Sang; Yoo, Hyang Sook
PA Korea Research Institute of Bioscience and Biotechnology, S. Korea
SO PCT Int. Appl., 112 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2005001126	A1	20050106	WO 2004-KR677	20040325
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2004107145	A	20041220	KR 2003-38034	20030612
	KR 2005050295	A	20050531	KR 2003-84001	20031125
	JP 2006526998	T	20061130	JP 2006-516902	20040325
PRAI	KR 2003-38034	A	20030612		
	KR 2003-84001	A	20031125		
	WO 2004-KR677	W	20040325		

AB A panel of expressed sequence tags (ESTs) that can be used as markers to diagnose gastric cancer and its metastases is identified. The genes can also be used as markers in screening for drugs for treatment of the disease (no data.). The genes from which these markers are derived are identified. Reagents for detecting expression of these genes can be incorporated into a diagnostic kit. The ESTs were identified by comparing patterns of gene expression in 12 gastric cancer cell lines and four non-cancerous gastric cell lines. Up- and down-regulated genes were identified.

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

IN Kim, Nam-Soon; Kim, Yong Sung; Lee, Ju-Yeon; Oh, Jung-Hwa; Park, Hong-Seog; Ahn, Hee-Young; Yoon, Sun-Young; Han, Yoonsoo; Kim, Sangsoo; ***Kim, Jeong-Min*** ; Byun, Sang-Soon; Noh, Seung-Moo; Song, Kyu-Sang; Yoo, Hyang Sook

IT Gene, animal
RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(***HSPA8*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)

IT Gene, animal
RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(***HSPB1*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)

IT Gene, animal
RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(***HSPCA*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)

IT Gene, animal

RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(***HSPCB*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)

L6 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 2
AN 2004:485515 CAPLUS <<LOGINID::20090617>>
DN 141:2160
TI Gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags
AU Kim, Nam-Soon; Hahn, Yoonsoo; Oh, Jung-Hwa; Lee, Ju-Yeon; Oh, Kyung-Jin; ***Kim, Jeong-Min*** ; Park, Hong-Seog; Kim, Sangsoo; Song, Kyu-Sang; Rho, Seung-Moo; Yoo, Hyang-Sook; Kim, Yong Sung
CS Laboratory of Human Genomics, Korea Research Institute of Bioscience and Biotechnology, Daejeon, 305-333, S. Korea
SO Genomics (2004), 83(6), 1024-1045
CODEN: GNMCEP; ISSN: 0888-7543
PB Elsevier Science
DT Journal
LA English
AB To understand the mol. mechanism assocd. with gastric carcinogenesis, genes expressed in gastric cancer cell lines and tissues were identified. Of 97,609 high-quality ESTs sequenced from 36 cDNA libraries, 92,545 were coalesced into 10,418 human Unigene clusters (Build 151). The gene expression profile was produced by counting the cluster frequencies in each library. Although the profiles of highly expressed genes varied greatly from library to library, those genes related to cell structure formation, heat shock proteins, the glycolysis pathway, and the signaling pathway were highly represented in human gastric cancer cell lines and in primary tumors. Conversely, the genes encoding Igs, ribosomal proteins, and digestive proteins were down-regulated in gastric cancer cell lines and tissues compared to normal tissues. The transcription levels of some of these genes were confirmed by RT-PCR. Genes related to cell adhesion, apoptosis, and cytoskeleton formation were particularly up-regulated in the gastric cancer cell lines established from malignant ascites compared to those from primary tumors. This comprehensive mol. profiling of human gastric cancer should be useful for elucidating the genetic events assocd. with human gastric cancer. [This abstr. record is one of 24 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
AU Kim, Nam-Soon; Hahn, Yoonsoo; Oh, Jung-Hwa; Lee, Ju-Yeon; Oh, Kyung-Jin; ***Kim, Jeong-Min*** ; Park, Hong-Seog; Kim, Sangsoo; Song, Kyu-Sang; Rho, Seung-Moo; Yoo, Hyang-Sook; Kim, Yong Sung
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 27, protein 1; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 70, protein 8; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 90; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)

L6 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:591378 CAPLUS <<LOGINID::20090617>>
DN 139:146183
TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species
IN Kim, Bum-joon; Kook, Yoon-ho; ***Kim, Jeong-mi***
PA Biomedlab Corporation, S. Korea
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species
IN Kim, Bum-joon; Kook, Yoon-ho; ***Kim, Jeong-mi***
AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .
ST primer mycobacteria heat shock protein ***hsp65*** gene
IT Nucleic acid amplification (method)
(DNA; primers for amplifying mycobacterial heat shock protein

HSP 65 gene and use for identifying mycobacterial species)

IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Diagnosis
(mol.; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium
Mycobacterium avium paratuberculosis
Mycobacterium bovis
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium leprae
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium microti
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium parafortuitum
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium simiae
Mycobacterium smegmatis

Mycobacterium szulgai
Mycobacterium terrae
Mycobacterium thermoresistibile
Mycobacterium triviale
Mycobacterium tuberculosis
Mycobacterium ulcerans
Mycobacterium vaccae
Mycobacterium wolinskyi
Nocardia carnea
RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
569432-52-6 569432-53-7 569432-54-8 569432-55-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-56-0
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPF3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-57-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPR3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569477-29-8
RL: PRP (Properties)
(unclaimed sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

=> s hsp65 and primer?
L7 173 HSP65 AND PRIMER?

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 93 DUP REM L7 (80 DUPLICATES REMOVED)

=> s l8 and (diagnos? or identif?) and mycobact?
L9 71 L8 AND (DIAGNOS? OR IDENTIF?) AND MYCOBACT?

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 71 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2009:116848 BIOSIS <<LOGINID::20090617>>
DN PREV200900116848
TI Multi-Probe Real-Time PCR ***Identification*** of Common ***Mycobacterium*** Species in Blood Culture Broth.
AU Foongladda, Suporn [Reprint Author]; Pholwat, Suporn; Eampokalap, Boonchuay; Kiratisin, Pattarachai; Sutthent, Ruengpung
CS Mahidol Univ, Fac Med, Siriraj Hosp, Dept Microbiol, 2 Prannok Rd, Bangkok 10700, Thailand
sisfm@mahidol.ac.th
SO Journal of Molecular Diagnostics, (JAN 2009) Vol. 11, No. 1, pp. 42-48.
ISSN: 1525-1578.
DT Article
LA English
ED Entered STN: 11 Feb 2009
Last Updated on STN: 11 Feb 2009
AB ***Mycobacterium*** tuberculosis complex, M. avium, and M. intracellulare are the most common causes of systemic bacterial infection in AIDS patients. To ***identify*** these ***mycobacterial*** isolates in primary blood culture broths, we developed a multiple hybridization probe-based real-time PCR assay using the LightCycler system. The ***primers*** were designed to amplify a 320-bp fragment of ***Mycobacterium*** 16S rRNA genes. Reaction specificity was evaluated using PCR amplification curves along with specific melting temperatures of probes on DNA extracted from 13 ***Mycobacterium*** species. In this study, results showed 100% accuracy for the selected bacterial panel. Detection limits were 350, 600, and 650 colony-forming unit (CFU)/ml blood culture broths for M. tuberculosis complex, M. avium, and M. intracellulare, respectively (I to 2 CFU/reaction). To evaluate clinical applicability, 341 acid-fast bacilli in blood culture broths were analyzed. in total, 327 (96%) were positively ***identified*** : 54.5% M. tuberculosis complex, 37.5% M. avium, and 3.8% M. intracellulare. Results can be available within 3 hours of receiving a broth sample, which makes this rapid and simple assay an attractive ***diagnostic*** tool for clinical use. (J Mol Diagn 2009, 11:42-48; DOI: 10.2353/jmoldx.2009.080081)

TI Multi-Probe Real-Time PCR ***Identification*** of Common ***Mycobacterium*** Species in Blood Culture Broth.

AB ***Mycobacterium*** tuberculosis complex, M. avium, and M. intracellulare are the most common causes of systemic bacterial infection in AIDS patients. To ***identify*** these ***mycobacterial*** isolates in primary blood culture broths, we developed a multiple hybridization probe-based real-time PCR assay using the LightCycler system. The ***primers*** were designed to amplify a 320-bp fragment of ***Mycobacterium*** 16S rRNA genes. Reaction specificity was evaluated using PCR amplification curves along with specific melting temperatures of probes on DNA extracted from 13 ***Mycobacterium*** species. In this study, results showed 100% accuracy for the selected bacterial panel. Detection limits were 350, 600, and 650. . . CFU/reaction). To evaluate clinical applicability, 341 acid-fast bacilli in blood culture broths were analyzed. in total, 327 (96%) were positively ***identified*** : 54.5% M. tuberculosis complex, 37.5% M. avium, and 3.8% M. intracellulare. Results can be available within 3 hours of receiving a broth sample, which makes this rapid and simple assay an attractive ***diagnostic*** tool for clinical use. (J Mol Diagn 2009, 11:42-48; DOI: 10.2353/jmoldx.2009.080081)

IT Major Concepts
Infection; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Diseases
mycobacterial infection: bacterial disease
Mycobacterium Infections (MeSH)

IT Chemicals & Biochemicals
16S rRNA gene; blood culture broth

ORGN . . .
Primates; Mammalia; Vertebrata; Chordata; Animalia

Organism Name
human (common): host

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium tuberculosis (species): pathogen
Mycobacterium avium (species): pathogen
Mycobacterium intracellulare (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** tuberculosis ***hsp65*** gene (***Mycobacteriaceae***)

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AN 2009:80424 BIOSIS <<LOGINID::20090617>>

DN PREV200900080424

TI rpoB sequence-based ***identification*** of ***Mycobacterium*** avium complex species.

AU Ben Salah, Iskandar; Adekambi, Toidi; Raoult, Didier; Drancourt, Michel [Reprint Author]

CS Univ Aix Marseille 2, Fac Med,Unite Rech Malad Infect and Trop Emergentes, IFR 48,UMR 6236, CNRS IRD, Marseille, France

Michel.Dfancourt@medecine.univ-mrs.fr
SO Microbiology (Reading), (DEC 2008) Vol. 154, No. Part 12, pp. 3715-3723. ISSN: 1350-0872.
DT Article
LA English
ED Entered STN: 22 Jan 2009
Last Updated on STN: 22 Jan 2009
AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing ***mycobacteria*** responsible for opportunistic infections and zoonoses. The ability to speciate MAC isolates in the clinical microbiology laboratory is critical for determining the organism implicated in clinical disease and for epidemiological investigation of the source of infection. Investigation of a 711 bp variable fragment of rpoB flanked by the Myco-F/Myco-R ***primers*** found a 0.7-5.1% divergence among MAC reference strains, with ***Mycobacterium*** chimaera and ***Mycobacterium*** intracellulare being the most closely related. Using a 0.7 % divergence cut-off, 83% of 100 clinical isolates, which had been previously ***identified*** by phenotypic characteristics and 16S-23S rDNA intergenic spacer (ITS) probing, were ***identified*** as M. avium, 8% as M. intracellulare and 2% as M. chimaera. The uniqueness of seven isolates, exhibiting < 99.3 % rpoB sequence similarity with MAC reference strains, was confirmed by 16S rDNA, ITS and ***hsp65*** sequencing and phylogenetic analyses. Partial rpoB gene sequencing using the Myco-F/Myco-R ***primers*** permits one-step ***identification*** of MAC isolates at the species level and the detection of potentially novel MAC species.
TI rpoB sequence-based ***identification*** of ***Mycobacterium*** avium complex species.
AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing ***mycobacteria*** responsible for opportunistic infections and zoonoses. The ability to speciate MAC isolates in the clinical microbiology laboratory is critical for. . . epidemiological investigation of the source of infection. Investigation of a 711 bp variable fragment of rpoB flanked by the Myco-F/Myco-R ***primers*** found a 0.7-5.1% divergence among MAC reference strains, with ***Mycobacterium*** chimaera and ***Mycobacterium*** intracellulare being the most closely related. Using a 0.7 % divergence cut-off, 83% of 100 clinical isolates, which had been previously ***identified*** by phenotypic characteristics and 16S-23S rDNA intergenic spacer (ITS) probing, were ***identified*** as M. avium, 8% as M. intracellulare and 2% as M. chimaera. The uniqueness of seven isolates, exhibiting < 99.3 % rpoB sequence similarity with MAC reference strains, was confirmed by 16S rDNA, ITS and ***hsp65*** sequencing and phylogenetic analyses. Partial rpoB gene sequencing using the Myco-F/Myco-R ***primers*** permits one-step ***identification*** of MAC isolates at the species level and the detection of potentially novel MAC species.
IT . . .
and Molecular Biophysics)
IT Diseases
infection: infectious disease
Infection (MeSH)
IT Chemicals & Biochemicals
rpoB; 16S-23S rDNA: intergenic spacer probing; Myco-F ***primer*** ; Myco-R ***primer***
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium avium (species): pathogen
Mycobacterium intracellulare (species): pathogen
Mycobacterium avium complex (species): pathogen
Mycobacterium chimaera (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Mycobacterium*** avium complex rpoB gene (***Mycobacteriaceae***)

L9 ANSWER 3 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2008:704929 BIOSIS <<LOGINID::20090617>>
DN PREV200800704928
TI ***Identification*** of individual DNA molecule of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis.
AU Chang, Po-Ling; Hsieh, Wen-Shyang; Chiang, Chia-Lien; Yen-Liberman, Belinda; Procop, Gary W.; Chang, Huan-Tsung [Reprint Author]; Ho, Hsin-Tsung
CS Natl Taiwan Univ, Dept Chem, Taipei 10764, Taiwan
changht@ntu.edu.tw; drho@ms2.mmh.org.tw
SO Talanta, (OCT 15 2008) Vol. 77, No. 1, pp. 182-188.
CODEN: TLNTA2. ISSN: 0039-9140.
DT Article
LA English
ED Entered STN: 3 Dec 2008
Last Updated on STN: 3 Dec 2008
AB The improvement of sensitivity and differentiation in rapidly ***identifying*** a small amount of ***mycobacteria*** in sputum has significant implications for reducing tuberculosis transmission. We previously applied the conventional PCR and capillary electrophoresis (CE) to establish the restriction fragment length polymorphism (RFLP) pattern of ***mycobacterial*** 65-kDa heat shock protein (***hsp65***) gene from colony specimens. However, the previous analysis did not provide enough sensitivity for sputum specimens in which the limitation of analysis might be hindered by PCR inhibitors and ***primer*** -dimers formation during amplification. In the current study, nested PCR (nPCR) had been redesigned for PCR-RFLP analysis (PRA) of ***mycobacterial*** ***hsp65*** gene using CE. The results show both ***Mycobacterium*** tuberculosis complex and ***mycobacteria*** other than tuberculosis could be ***identified*** in the presence of PCR inhibitors. The interference due to ***primer*** -dimers was also minimized. Based on the Poisson distribution, the repeatability of single DNA molecule detection was greatly affected by sampling probability and might be improved significantly by increasing the sample loading. The PRA using nPCR and CE is not only able to detect the individual ***mycobacterial*** DNA molecule but also potentially differentiate the species. (c) 2008 Elsevier B.V. All rights reserved.
TI ***Identification*** of individual DNA molecule of ***Mycobacterium*** tuberculosis by nested PCR-RFLP and capillary electrophoresis.
AB The improvement of sensitivity and differentiation in rapidly ***identifying*** a small amount of ***mycobacteria*** in sputum has

significant implications for reducing tuberculosis transmission. We previously applied the conventional PCR and capillary electrophoresis (CE) to establish the restriction fragment length polymorphism (RFLP) pattern of ***mycobacterial*** 65-kDa heat shock protein (***hsp65***) gene from colony specimens. However, the previous analysis did not provide enough sensitivity for sputum specimens in which the limitation of analysis might be hindered by PCR inhibitors and ***primer*** -dimers formation during amplification. In the current study, nested PCR (nPCR) had been redesigned for PCR-RFLP analysis (PRA) of ***mycobacterial*** ***hsp65*** gene using CE. The results show both ***Mycobacterium*** tuberculosis complex and ***mycobacteria*** other than tuberculosis could be ***identified*** in the presence of PCR inhibitors. The interference due to ***primer*** -dimers was also minimized. Based on the Poisson distribution, the repeatability of single DNA molecule detection was greatly affected by sampling. . . significantly by increasing the sample loading. The PRA using nPCR and CE is not only able to detect the individual ***mycobacterial*** DNA molecule but also potentially differentiate the species. (c) 2008 Elsevier B.V. All rights reserved.

IT . . .

Structures, & Systems of Organisms

sputum

IT Diseases

tuberculosis: bacterial disease, transmission

Tuberculosis (MeSH)

IT Chemicals & Biochemicals

PCR inhibitor; DNA: ***identification*** ; ***primer*** -dimer: formation

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium tuberculosis (species)

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** tuberculosis ***hsp65*** gene [***Mycobacterium*** tuberculosis 65-kDa heat shock protein gene] (***Mycobacteriaceae***)

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AN 2008:586534 BIOSIS <<LOGINID::20090617>>

DN PREV200800586533

TI ***Mycobacterium*** porcinum strains isolated from bovine bulk milk: Implications for ***Mycobacterium*** avium subsp paratuberculosis detection by PCR and culture.

AU Taddei, R. [Reprint Author]; Barbieri, I.; Pacciarini, M. L.; Fallacara, F.; Belletti, G. L.; Arrigoni, N.

CS Ist Zooprofilattico Sperimentale Lombardia and Emil, Sez Forli, Via Marchini 1, I-47100 Forli, Italy
roberta.taddei@bs.izs.it

SO Veterinary Microbiology, (AUG 25 2008) Vol. 130, No. 3-4, pp. 338-347. CODEN: VMICDQ. ISSN: 0378-1135.

DT Article

LA English

ED Entered STN: 22 Oct 2008

Last Updated on STN: 22 Oct 2008

AB In this study, the isolation of 52 ***mycobactin*** -independent fast growing ***mycobacteria*** from 631 bulk milk samples (8.2%), is reported. These strains, isolated during a bulk milk survey for ***Mycobacterium*** avium subsp. paratuberculosis (Map), strongly affected Map detection both by PCR and by culture, as they gave a positive IS900 PCR signal and resulted to totally inhibit the growth of Map when spotted on HEYM slants already inoculated with 200 mu 1 of 10-fold dilutions containing from 5 x 10 to 5 x 10(3) Map cells/ml. 16S rRNA gene sequencing, using the MicroSeq 500 16S rDNA Bacterial Sequencing Kit (Applied Biosystems), was performed on a subset of six strains, ***identifying*** ***Mycobacterium*** porcinum with 100% homology in all six cases. The 52 strains were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of the ***hsp65*** gene, which confirmed the ***identification*** of M. porcinum for all the isolates. Using specific ***primers*** designed on the Map-IS900 sequence and on the M. porcinum sequence determined in this study, a 1385 bp sequence from the M. porcinum genome was characterized. This IS900-like sequence showed 82% homology with Map IS900. From our findings the following results emerged: (a) any culture showing one or more M. porcinum colonies represents a potential "false negative" result and should therefore be considered as contaminated; (b) IS900-like elements could be more widespread than was previously thought; (c) IS900 PCR positive results should be interpreted cautiously, as confirmed by the evidence that the ***primer*** pair used in this study resulted not to be specific (C) 2008 Elsevier B.V. All rights reserved.

TI ***Mycobacterium*** porcinum strains isolated from bovine bulk milk: Implications for ***Mycobacterium*** avium subsp paratuberculosis detection by PCR and culture.

AB In this study, the isolation of 52 ***mycobactin*** -independent fast growing ***mycobacteria*** from 631 bulk milk samples (8.2%), is reported. These strains, isolated during a bulk milk survey for ***Mycobacterium*** avium subsp. paratuberculosis (Map), strongly affected Map detection both by PCR and by culture, as they gave a positive IS900. . . sequencing, using the MicroSeq 500 16S rDNA Bacterial Sequencing Kit (Applied Biosystems), was performed on a subset of six strains, ***identifying*** ***Mycobacterium*** porcinum with 100% homology in all six cases. The 52 strains were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of the ***hsp65*** gene, which confirmed the ***identification*** of M. porcinum for all the isolates. Using specific ***primers*** designed on the Map-IS900 sequence and on the M. porcinum sequence determined in this study, a 1385 bp sequence from. . . than was previously thought; (c) IS900 PCR positive results should be interpreted cautiously, as confirmed by the evidence that the ***primer*** pair used in this study resulted not to be specific (C) 2008 Elsevier B.V. All rights reserved.

ORGN . . .
Chordata; Animalia
Organism Name
bovine (common): host
Taxa Notes
Animals, Artiodactyls, Chordates, Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium avium paratuberculosis (subspecies): pathogen
Mycobacterium porcinum (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 5 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:529420 BIOSIS <<LOGINID::20090617>>
DN PREV200700528890
TI ***Mycobacterium*** species ***identification*** - A new approach via dnaJ gene sequencing.
AU Yamada-Noda, Makiko; Ohkusu, Kiyofumi; Hata, Hiroyuki; Shah, Mohammad Monir; Nhung, Pham Hong; Sun, Xiao Song; Hayashi, Masahiro; Ezaki, Takayuki [Reprint Author]
CS Gifu Univ, Grad Sch Med, Dept Microbiol Regenerat and Adv Med Sci, 1-1 Yanagido, Gifu 5011194, Japan
tezaki@gifu-u.ac.jp
SO Systematic and Applied Microbiology, (SEP 2007) Vol. 30, No. 6, pp. 453-462.
CODEN: SAMIDF. ISSN: 0723-2020.
DT Article
LA English
ED Entered STN: 10 Oct 2007
Last Updated on STN: 10 Oct 2007
AB The availability of the dnaJ] gene for ***identifying*** ***Mycobacterium*** species was examined by analyzing the complete dnaJ1 sequences (approximately 1200 bp) of 56 species (54 of them were type strains) and comparing sequence homologies with those of the 16S rRNA gene and other housekeeping genes (rpoB, ***hsp65***). Among the 56 ***Mycobacterium*** species, the mean sequence similarity of the dnaJ1 gene (80.4%) was significantly less than that of the 16S rRNA, rpoB and ***hsp65*** genes (96.6 %, 91.3 % and 9 1.1 %, respectively), indicating a high discriminatory power of the dnaJ1 gene. Seventy-one clinical isolates were correctly clustered to the corresponding type strains, showing isolates belonging to the same species. In order to propose a method for strain ***identification*** , we ***identified*** an area with a high degree of polymorphism, bordered by conserved sequences, that can be used as universal ***primers*** for PCR amplification and sequencing. The sequence of this fragment (approximately 350bp) allows accurate species ***identification*** and may be used as a new tool for the ***identification*** of ***Mycobacterium*** species. (c) 2007 Published by Elsevier GmbH.
TI ***Mycobacterium*** species ***identification*** - A new approach via dnaJ gene sequencing.
AB The availability of the dnaJ] gene for ***identifying*** ***Mycobacterium*** species was examined by analyzing the complete dnaJ1 sequences (approximately 1200 bp) of 56 species (54 of them were type strains) and comparing sequence homologies with those of the 16S rRNA gene and other housekeeping genes (rpoB, ***hsp65***). Among the 56 ***Mycobacterium*** species, the mean sequence similarity of the dnaJ1 gene (80.4%) was significantly less than that of the 16S rRNA, rpoB and

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ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium tuberculosis (species)
Mycobacterium avium (species)
Mycobacterium kansasii (species)
Mycobacterium (genus)
Mycobacterium gastri (species)
Mycobacterium ulcerans (species)
Mycobacterium mucogenicum (species)
Mycobacterium parafortuitum (species)
Mycobacterium genavense (species)
Mycobacterium scrilaceum (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms
ORGN Classifier
Nocardioform Actinomycetes 08810
Super Taxa
Actinomycetes and Related Organisms; Eubacteria; Bacteria;. . .
GEN ***Mycobacterium*** dnaJ gene (***Mycobacteriaceae***): polymorphism; ***Mycobacterium*** rpoB gene (***Mycobacteriaceae***): polymorphism; ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***): polymorphism

L9 ANSWER 6 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:419642 BIOSIS <<LOGINID::20090617>>
DN PREV200700424384
TI Detection of ***Mycobacterium*** species distribution in the sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province. Original Title: ELAZIG YORESINDE TUBERKULOZLU HASTALARIN BALGAM ORNEKLERINDE MIKOBAKTERI TUR DAGILIMININ PCR-RFLP YONTEMI ILE BELIRLENMESI.
AU Agacayak, Ahmet [Reprint Author]; Bulut, Yasemin; Seyrek, Adnan
CS Firat Univ, Tip Fak, Mikrobiyoloji and Klin Mikrobiyoloji Anabilim Dali, Elazig, Turkey
ybulut@firat.edu.tr
SO Mikrobiyoloji Bulteni, (APR 2007) Vol. 41, No. 2, pp. 203-209. CODEN: MIBUBI. ISSN: 0374-9096.
DT Article
LA Turkish
ED Entered STN: 8 Aug 2007
Last Updated on STN: 7 Nov 2007

AB The aim of this study was to detect the ***Mycobacterium*** species in the sputum samples collected from tuberculosis patients in Elazig province (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) method. A total of 60 samples from patients (32 male, 28 female) who were ***diagnosed*** as tuberculosis by culture positivity at Elazig Tuberculosis Control Dispensary, were included to the study. After DNA extraction and isolation from the samples, gene region encoding for 65 kDa protein of ***mycobacteria*** was amplified with specific ***primers*** (first step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2; 5'-AGC TGC AGC CCA AAG GTG TT- 3', second step ***primers*** : TB1 and TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using seminested PCR method. According to ***hsp65*** gene region amplification, 51 (85%) samples yielded positive results, while nine (15%) samples could not be ***identified*** . Of 51 samples, 44 (86.3%) were ***identified*** as M.tuberculosis complex, four (7.8%) were M.scrofulaceum, two (3.9%) were M.avium and one (1.9%) was M.intracellulare, in the restriction assay by HaeIII of the PCR products. In order to ***identify*** the species of M.tuberculosis complex, gyrB gene region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR products were restricted by RsaI and TaqI enzymes. In this assay, 34 (77.3%), eight (18.2%), one (2.3%) and one (2.3%) of the 44 M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, respectively. Our data indicated that at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by molecular methods and clarifying their resistance patterns against antituberculous drugs are needed for the effective control of tuberculosis.

TI Detection of ***Mycobacterium*** species distribution in the sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province. Original Title: ELAZIG YORESINDE TUBERKULOZLU. . .

AB The aim of this study was to detect the ***Mycobacterium*** species in the sputum samples collected from tuberculosis patients in Elazig province (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) method. A total of 60 samples from patients (32 male, 28 female) who were ***diagnosed*** as tuberculosis by culture positivity at Elazig Tuberculosis Control Dispensary, were included to the study. After DNA extraction and isolation from the samples, gene region encoding for 65 kDa protein of ***mycobacteria*** was amplified with specific ***primers*** (first step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2; 5'-AGC TGC AGC CCA AAG GTG TT- 3', second step ***primers*** : TB1 and TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using seminested PCR method. According to ***hsp65*** gene region amplification, 51 (85%) samples yielded positive results, while nine (15%) samples could not be ***identified*** . Of 51 samples, 44 (86.3%) were ***identified*** as M.tuberculosis complex, four (7.8%) were M.scrofulaceum, two (3.9%) were M.avium and one (1.9%) was M.intracellulare, in the restriction assay by HaeIII of the PCR products. In order to ***identify*** the species of M.tuberculosis complex, gyrB gene region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR. . . M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, respectively. Our data indicated that

at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by molecular methods and clarifying their resistance patterns against antituberculous drugs are needed. . .

IT . . .
(Biochemistry and Molecular Biophysics)

IT Parts, Structures, & Systems of Organisms
sputum

IT Diseases
tuberculosis: bacterial disease, infectious disease, epidemiology, ***diagnosis***
Tuberculosis (MeSH)

IT Chemicals & Biochemicals
DNA

ORGN . . .
Vertebrata; Chordata; Animalia

Organism Name
human (common): host, female, male

Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium tuberculosis (species): pathogen
Mycobacterium bovis (species): pathogen
Mycobacterium avium (species): pathogen
Mycobacterium intracellulare (species): pathogen
Mycobacterium scrofulaceum (species): pathogen
Mycobacterium microti (species): pathogen
Mycobacterium africanum (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 7 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:36655 BIOSIS <<LOGINID::20090617>>
DN PREV200700037125
TI Study of PCR for direct detection and ***identification*** of ***mycobacteria*** in skin specimens.
AU Wang Hong-sheng [Reprint Author]; Li Xiao-jie; Wu Qin-xue; Cui Pan-gen; Liu Xun-quan
CS Chinese Acad Med Sci, Inst Dermatol, Nanjing 210042, Peoples R China
wuqx2003@hotmail.com
SO Zhonghua Pifuke Zazhi, (OCT 2006) Vol. 39, No. 10, pp. 593-595.
CODEN: CHFTAJ. ISSN: 0412-4030.
DT Article
LA Chinese
ED Entered STN: 27 Dec 2006
Last Updated on STN: 27 Dec 2006
AB Objective To study the possibility of direct detection and ***identification*** of ***mycobacteria*** by PCR in skin specimens.Methods The comparison of PCR with in vitro culture of M smegmatis was conducted at three levels. First, serial dilutions of M. sinegmatis DNA was amplified with ***primers*** aiming at

hsp65 gene to testify the sensitivity of PCR for
mycobacterial detection, and the same dilutions of suspension of M
smegmatis was inoculated in Lowenstein-Jensen medium to assessed the sensitivity of in vitro culture. Secondly, the results of detecting simulant clinical specimens by PCR with or without pretreatment were compared with those by in vitro culture. Thirdly, the results of detecting 37 clinical skin specimens suspected to be infected with ***mycobacteria*** by PCR with or without pretreatment were compared with those by in vitro culture.Results The sensitivity of both PCR and in vitro culture for detection of serial dilutions of bacterial suspension of M. smegmatis was 1 x 10(2) cells/mL. The detection rates of PCR for simulant clinical skin specimen at 1 x 10(2) cells/mL with and without pretreatment were 60% and 0 respectively, and the detection rates of in vitro culture were 80% and 100%, respectively. The detection rate of PCR was 100% for simulant clinical skin specimens at 1 x 10(3) cells/mL. From the 37 clinical skin specimens, 7 and 2 positive cases were detected by PCR with and without pretreatment respectively, however, 9 positive cases were detected by in vitro culture.Conclusion With the pretreatment of clinical skin specimens, the sensitivity of PCR approximates 80% and the time needed for detection is obviously shortened.

TI Study of PCR for direct detection and ***identification*** of ***mycobacteria*** in skin specimens.

AB Objective To study the possibility of direct detection and ***identification*** of ***mycobacteria*** by PCR in skin specimens.Methods The comparison of PCR with in vitro culture of M smegmatis was conducted at three levels. First, serial dilutions of M. sinegmatis DNA was amplified with ***primers*** aiming at ***hsp65*** gene to testify the sensitivity of PCR for ***mycobacterial*** detection, and the same dilutions of suspension of M
smegmatis was inoculated in Lowenstein-Jensen medium to assessed the sensitivity of. . . with those by in vitro culture. Thirdly, the results of detecting 37 clinical skin specimens suspected to be infected with ***mycobacteria*** by PCR with or without pretreatment were compared with those by in vitro culture.Results The sensitivity of both PCR and. . .

ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacteria smegmatis (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacteria*** smegmatis ***hsp65*** gene (***Mycobacteriaceae***)

L9 ANSWER 8 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2006:321383 BIOSIS <<LOGINID::20090617>>
DN PREV200600320304
TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum polymerase chain reaction.
AU Tzen, Chi-Yuan; Wu, Tsu-Yen; Tzen, Chin-Yuan [Reprint Author]
CS Mackay Mem Hosp, Dept Pathol, 45 Minsheng Rd, Taipei, Taiwan
jeffrey@ms2.mmh.org.tw

SO Journal of the Formosan Medical Association, (APR 2006) Vol. 105, No. 4, pp. 290-298.
ISSN: 0929-6646.
DT Article
LA English
ED Entered STN: 21 Jun 2006
Last Updated on STN: 21 Jun 2006
AB Background: The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease.Methods: Pan ***mycobacterium*** ***primers*** of the 65-kDa heat shock protein gene (***Hsp65***) were used in a polymerase chain reaction (PCR) to examine 12 surgical ly-resected, formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank.Results: ***Mycobacterial*** DNA was found in specimens from three of 11 patients. M. mucogenicum was ***identified*** in a specimen from one patient and M. tuberculosis in two, but Map was not ***identified*** in any.Conclusion: ***Hsp65*** -based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a ***diagnosis*** or suspicion of Crohn's disease. This approach may have a therapeutic implication. [J Formos Med Assoc 2006;105(4):290-298].
TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum polymerase chain reaction.
AB Background: The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease.Methods: Pan ***mycobacterium*** ***primers*** of the 65-kDa heat shock protein gene (***Hsp65***) were used in a polymerase chain reaction (PCR) to examine 12 surgical ly-resected, formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank.Results: ***Mycobacterial*** DNA was found in specimens from three of 11 patients. M. mucogenicum was ***identified*** in a specimen from one patient and M. tuberculosis in two, but Map was not ***identified*** in any.Conclusion: ***Hsp65*** -based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a ***diagnosis*** or suspicion of Crohn's disease. This approach may have a therapeutic implication. [J Formos Med Assoc 2006;105(4):290-298].
ORGN . . .
Organism Name
human (common): adult, middle age, host, female, male
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium tuberculosis (species): pathogen

Mycobacterium avium paratuberculosis (subspecies): pathogen
Mycobacterium mucogenicum (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Mycobacterium*** avium paratuberculosis ***Hsp65*** gene [
Mycobacterium avium paratuberculosis heat shock protein 65 gene]
(
Mycobacteriaceae)

L9 ANSWER 9 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2003:556261 BIOSIS <<LOGINID::20090617>>
DN PREV200300556972
TI ***Identification*** of ***Mycobacterium*** species and characterization of strains using a labchip (microfluidic) instrument.
AU Cooksey, R. C. [Reprint Author]; Limor, J. R. [Reprint Author]
CS CDC, Atlanta, GA, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. U-029.
http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 26 Nov 2003
Last Updated on STN: 26 Nov 2003
AB We developed schemes for rapid ***identification*** of ***Mycobacterium*** species and strain typing using a labchip instrument (Agilent Model 2100 Bioanalyzer) which uses electrokinetic forces to drive samples through chip microchannels (microfluidics), enabling real-time resolution and detection of sample components. A 439-bp region of ***hsp65*** that has sequence polymorphisms specific for most ***mycobacterial*** species has been characterized by PCR restriction analysis (PRA) with BstEII or HaeIII as a species ***identification*** tool. We performed PRA in duplicate, using 2 strains each of 13 species, and analyzing 1 ul of each digest. Fragment sizes (bp) determined automatically by the instrument were consistently smaller than the correct sizes for each of the species as determined by sequence analysis (mean variance, 7.5%) but varied by ltoreq6 bp for specific fragments in duplicate runs. M. tuberculosis isolates were typed with the labchip instrument by using ***mycobacterial*** interspersed repetitive unit (MIRU) typing, a variable number tandem repeat typing method which determines the number of copies of repeated units at 12 loci scattered throughout the genome based on product size after PCR amplification. Eleven isolates with 1 to 6 repeat copies at each locus were examined. Sizes were smaller by a mean of 4% compared to correct sizes predicted by sequence analysis, varied on duplicate runs by ltoreq5 bp, and could be used to correctly ***identify*** all strain types. Nontuberculous ***Mycobacterium*** species were typed using randomly amplified polymorphic DNA (RAPD) electrophoresis on the labchip instrument. PCR using a single 10-mer ***primer*** and low annealing temperature (37degreeC) was performed using 5 clusters each of M. chelonae, M. abscessus, and M. mucogenicum (13 isolates of each species) and 3 clusters of M. avium (11 isolates). All clusters were distinguished when patterns were compared to results of pulsed-field gel electrophoresis. RAPD

patterns for 1 M. abscessus strain were unchanged when we tested DNA from 2 cultures or DNA extracted on 6 different days from the same culture. The labchip instrument is a versatile alternative for sizing ***mycobacterial*** DNA fragments.

TI ***Identification*** of ***Mycobacterium*** species and characterization of strains using a labchip (microfluidic) instrument.

AB We developed schemes for rapid ***identification*** of ***Mycobacterium*** species and strain typing using a labchip instrument (Agilent Model 2100 Bioanalyzer) which uses electrokinetic forces to drive samples through chip microchannels (microfluidics), enabling real-time resolution and detection of sample components. A 439-bp region of ***hsp65*** that has sequence polymorphisms specific for most ***mycobacterial*** species has been characterized by PCR restriction analysis (PRA) with BstEII or HaeIII as a species ***identification*** tool. We performed PRA in duplicate, using 2 strains each of 13 species, and analyzing 1 ul of each digest.. . . by ltoreq6 bp for specific fragments in duplicate runs. M. tuberculosis isolates were typed with the labchip instrument by using ***mycobacterial*** interspersed repetitive unit (MIRU) typing, a variable number tandem repeat typing method which determines the number of copies of repeated. . . to correct sizes predicted by sequence analysis, varied on duplicate runs by ltoreq5 bp, and could be used to correctly ***identify*** all strain types. Nontuberculous ***Mycobacterium*** species were typed using randomly amplified polymorphic DNA (RAPD) electrophoresis on the labchip instrument. PCR using a single 10-mer ***primer*** and low annealing temperature (37degreeC) was performed using 5 clusters each of M. chelonae, M. abscessus, and M. mucogenicum (13. . . or DNA extracted on 6 different days from the same culture. The labchip instrument is a versatile alternative for sizing ***mycobacterial*** DNA fragments.

IT Major Concepts
Equipment Apparatus Devices and Instrumentation; Human Medicine (Medical Sciences); Infection; Methods and Techniques

IT Diseases
mycobacterial infection: bacterial disease
Mycobacterium Infections (MeSH)

IT Chemicals & Biochemicals
DNA: analysis, extraction, fragment sizing

IT Methods & Equipment
PCR [polymerase chain reaction]: genetic techniques, laboratory techniques; labchip (microfluidic) instrument: laboratory equipment; ***mycobacterial*** interspersed repetitive unit typing: clinical techniques, ***diagnostic*** techniques, genetic techniques, laboratory techniques; restriction analysis: genetic techniques, laboratory techniques

IT Miscellaneous Descriptors
annealing temperatures; ***diagnostics*** ; medical bacteriology; methodology

ORGN . . .
Taxa
Primates; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
human (common)
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium abcessus (species): pathogen
Mycobacterium avium (species): pathogen
Mycobacterium chelonae (species): pathogen
Mycobacterium mucogenicum (species): pathogen
Mycobacterium spp. (species): pathogen, species
identification methods, strain characterization methods
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 10 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2003:518694 BIOSIS <<LOGINID::20090617>>
DN PREV200300520305
TI Rapid ***identification*** of ***Mycobacterium*** species by ***hsp65*** partial gene sequence.
AU McNabb, A. [Reprint Author]; Eisler, D. [Reprint Author]; Adie, K. [Reprint Author]; Amos, M. [Reprint Author]; Rodrigues, M. [Reprint Author]; Isaac-Renton, J. [Reprint Author]
CS British Columbia Centre for Disease Control, Vancouver, BC, Canada
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. C-220.
http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003
AB Currently, ***Mycobacterium*** species are ***identified*** using biochemical tests, mycolic acid analysis and commercial or in-house molecular methods. These methods vary in time, labour, cost, efficacy and adequacy, with some requiring a stepwise process incurring further cost or delay. In 1993 Telenti et al. reported an REA ***identification*** method for ***mycobacteria*** based on a 441bp ***hsp65*** fragment. Although an important break- through in ***mycobacteria*** ***identification*** , the technique is not without technical and interpretative difficulties. DNA sequencing of the Telenti fragment has demonstrated great promise for ***identifying*** ***mycobacteria*** , but previous investigations have been of limited scope. We amplified, using the Telenti ***primers*** , 78 ***mycobacteria*** putative and valid type strains, optimized and sequenced the 401nt region between the ***primers*** and loaded these sequences into a local BLAST search program to act as a reference library. This library was challenged with 328 isolates encompassing 28 ***Mycobacterium*** species ***identified*** by biochemical tests and/or commercial probes. ***hsp65*** analysis corroborated the ***identification*** of 274/328 (83.5%) of the isolates. All isolates of M. branderi, M. flavescens, M. gordonae, M. lentiflavum, M. marinum, M. mucogenicum, M. obuense, M. szulgai, M. thermoresistible, M. tuberculosis, or M. xenopi, were concordant. 71/72 MAC isolates ***identified*** as M. avium(54) or M. intracellulare(17) and 49 M. gordonae isolates were assigned to

three groups, type I(15), type 2(22) or type 3(12) as per Brunello et al. Of the 54 discordant isolates 21 purported M. chelonae were ***identified*** by ***hsp65*** as M. abscessus(17) or M. mucogenicum(4), 12 purported M. fortuitum isolates were ***identified*** as M. chelonae(1), M. peregrinum(10) or M. mucogenicum(1) and 21 isolates were associated with the M. terrae complex (6), other valid or putative species(8) or were un-assigned(7). We conclude that ***hsp65*** gene sequence is a reliable means for the routine ***identification*** of ***mycobacteria*** ; it is rapid (2 days), does not require mature cultures, is cost effective (approximately dollar sign30USD) and is capable of precise and broad-spectrum ***identifications*** .

TI Rapid ***identification*** of ***Mycobacterium*** species by ***hsp65*** partial gene sequence.

AB Currently, ***Mycobacterium*** species are ***identified*** using biochemical tests, mycolic acid analysis and commercial or in-house molecular methods. These methods vary in time, labour, cost, efficacy. . . adequacy, with some requiring a stepwise process incurring further cost or delay. In 1993 Telenti et al. reported an REA ***identification*** method for ***mycobacteria*** based on a 441bp ***hsp65*** fragment. Although an important break- through in ***mycobacteria*** ***identification*** , the technique is not without technical and interpretative difficulties. DNA sequencing of the Telenti fragment has demonstrated great promise for ***identifying*** ***mycobacteria*** , but previous investigations have been of limited scope. We amplified, using the Telenti ***primers*** , 78 ***mycobacteria*** putative and valid type strains, optimized and sequenced the 401nt region between the ***primers*** and loaded these sequences into a local BLAST search program to act as a reference library. This library was challenged with 328 isolates encompassing 28 ***Mycobacterium*** species ***identified*** by biochemical tests and/or commercial probes. ***hsp65*** analysis corroborated the ***identification*** of 274/328 (83.5%) of the isolates. All isolates of M. branderi, M. flavescens, M. gordonae, M. lentiflavum, M. marinum, M. mucogenicum, M. obuense, M. szulgai, M. thermoresistible, M. tuberculosis, or M. xenopi, were concordant. 71/72 MAC isolates ***identified*** as M. avium(54) or M. intracellulare(17) and 49 M. gordonae isolates were assigned to three groups, type I(15), type 2(22) or type 3(12) as per Brunello et al. Of the 54 discordant isolates 21 purported M. chelonae were ***identified*** by ***hsp65*** as M. abscessus(17) or M. mucogenicum(4), 12 purported M. fortuitum isolates were ***identified*** as M. chelonae(1), M. peregrinum(10) or M. mucogenicum(1) and 21 isolates were associated with the M. terrae complex (6), other valid or putative species(8) or were un-assigned(7). We conclude that ***hsp65*** gene sequence is a reliable means for the routine ***identification*** of ***mycobacteria*** ; it is rapid (2 days), does not require mature cultures, is cost effective (approximately dollar sign30USD) and is capable of precise and broad-spectrum ***identifications*** .

IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Chemicals & Biochemicals
Telenti ***primers***

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium (genus): ***identification***
Mycobacterium avium (species)
Mycobacterium branderi (species)
Mycobacterium chelonae (species)
Mycobacterium flavescens (species)
Mycobacterium gordonae (species)
Mycobacterium intracellular (species)
Mycobacterium lentiflavum (species)
Mycobacterium marinum (species)
Mycobacterium mucogenicum (species)
Mycobacterium obuense (species)
Mycobacterium peregrinum (species)
Mycobacterium sp. (species)
Mycobacterium szulgai (species)
Mycobacterium terrae (species)
Mycobacterium thermoresistible (species)
Mycobacterium tuberculosis (species)
Mycobacterium xenopi (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***hsp65*** gene

L9 ANSWER 11 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2002:188724 BIOSIS <<LOGINID::20090617>>
DN PREV200200188724
TI Comparison of biotyping and PCR restriction analysis (PRA) for species ***identification*** (Sps-ID) of non-tuberculous ***mycobacteria*** (NTM) in a reference laboratory in Brazil.
AU Ferrazoli, L. [Reprint author]; Silva, E. C. [Reprint author]; Martins, M. C. [Reprint author]; Ueki, S. M. [Reprint author]; Telles, M. A. S. [Reprint author]; Smole, S. C.; Leao, S. C.; Arbeit, R. D.
CS Institut Adolfo Lutz, Sao Paulo, Brazil
SO Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 206. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 13 Mar 2002
Last Updated on STN: 13 Mar 2002
AB Background: Conventional biotyping for Sps-ID of NTM requires up to 4 weeks and may delay appropriate therapy for NTM infections. This study compared Sps-ID by biotyping with PRA of ***hsp65*** , the gene encoding the 65 kDa heat shock protein, as per Telenti et al. 1993. Methods: From Jan 1 to Sept 30, 2000, a total of 298 isolates of NTM were processed at Institute Adolfo Lutz, Sao Paulo, Brazil; 158 were analyzed by both methods. For PRA, a 439 bp fragment of ***hsp65*** was amplified using ***primers*** TB11 and TB12, digested with HaeIII and with BstII, the digests resolved by electrophoresis in 4% agarose, and the patterns compared with the available database (http://www.hospvd.ch:8005). Results: Both methods agreed for 104 (64%) isolates, of which 60 were M. avium complex (MAC); 32, M. kansasii; 6, M. fortuitum; 4, M. gordonae; and

2, M. marinum. Biotyping was inconclusive for 13 (8%) isolates, of which PRA indicated 3 were MAC and 3 were M. kansasii. For 15 (9%) isolates, PRA yielded patterns not in the current databases; of these, biotyping indicated that 7 isolates representing two PRA patterns were M. gordonae. For 26 (16%) isolates, the two methods gave different Sps-ID. The non-concordant isolates are being resolved by sequencing the entire amplicon from ***hsp65*** . Conclusions: PRA provides rapid and reliable Sps-ID for the majority of NTM isolates encountered in a clinical reference laboratory. This should continue to improve as the database of known profiles expands. Further studies, including nucleotide sequencing of the PCR product are in progress to resolve those instances in which PRA and conventional biotyping disagree.

TI Comparison of biotyping and PCR restriction analysis (PRA) for species ***identification*** (Sps-ID) of non-tuberculous ***mycobacteria*** (NTM) in a reference laboratory in Brazil.

AB. . . to 4 weeks and may delay appropriate therapy for NTM infections. This study compared Sps-ID by biotyping with PRA of ***hsp65*** , the gene encoding the 65 kDa heat shock protein, as per Telenti et al. 1993. Methods: From Jan 1 to. . . at Institute Adolfo Lutz, Sao Paulo, Brazil; 158 were analyzed by both methods. For PRA, a 439 bp fragment of ***hsp65*** was amplified using ***primers*** TB11 and TB12, digested with HaeIII and with BstII, the digests resolved by electrophoresis in 4% agarose, and the patterns. . . (16%) isolates, the two methods gave different Sps-ID. The non-concordant isolates are being resolved by sequencing the entire amplicon from ***hsp65*** . Conclusions: PRA provides rapid and reliable Sps-ID for the majority of NTM isolates encountered in a clinical reference laboratory. This. . .

IT . . .
method, applications, molecular method; polymerase chain reaction restriction analysis technique: analytical method, applications, molecular method

IT Miscellaneous Descriptors
bacterial species ***identification*** : methodologies; clinical reference laboratories; databases; medical ***diagnostics*** ; medical microbiology; therapeutics; Meeting Abstract

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium spp.: ***identification*** methods, non-tuberculous, pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 12 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2001:409363 BIOSIS <<LOGINID::20090617>>

DN PREV200100409363

TI The DNA probe and PCR assay as useful tools to control an acid fast bacteria-dependent biotechnological process.

AU Brzostek, Anna M. [Reprint author]; Pawlowicz, Marek; Dziadek, Jaroslaw [Reprint author]

CS Department of Genetics of Microorganisms, Centre for Microbiology and Virology, Polish Academy of Sciences, 106, Lodowa St., 93-232, Lodz, Poland

SO Acta Microbiologica Polonica, (2001) Vol. 50, No. 1, pp. 37-44. print.
ISSN: 0137-1320.
DT Article
LA English
ED Entered STN: 29 Aug 2001
Last Updated on STN: 22 Feb 2002
AB Specific DNA probe has been developed for fast-growing, ***mycobacterial*** mutants able to selectively biotransform side chain of plant sterols. The PCR assay, using ***primers*** complementary to the sequence of the probe, was shown to distinguish biotechnological mutants from other fast-growing ***mycobacteria*** . Moreover, the species ***identification*** of biotechnological strains was done using PCR-restriction analysis based on amplification and digestion of the inner part of ***hsp65*** gene (PRA-assay) as well as 16S rRNA sequencing.
AB Specific DNA probe has been developed for fast-growing, ***mycobacterial*** mutants able to selectively biotransform side chain of plant sterols. The PCR assay, using ***primers*** complementary to the sequence of the probe, was shown to distinguish biotechnological mutants from other fast-growing ***mycobacteria*** . Moreover, the species ***identification*** of biotechnological strains was done using PCR-restriction analysis based on amplification and digestion of the inner part of ***hsp65*** gene (PRA-assay) as well as 16S rRNA sequencing.
ORGN Classifier
Bacteria 05000
Super Taxa
Microorganisms
Organism Name
bacteria
Taxa Notes
Bacteria, Eubacteria, Microorganisms
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
mycobacteria
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***)

L9 ANSWER 13 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1999:133687 BIOSIS <<LOGINID::20090617>>
DN PREV199900133687
TI Use of restriction enzyme analysis of amplified DNA coding for the ***hsp65*** gene and polymerase chain reaction with universal ***primer*** for rapid differentiation of ***Mycobacterium*** species in the clinical laboratory.
AU Bahrmand, Ahmad R. [Reprint author]; Bakayeva, Tamara G.; Bakayev, Valery V.
CS Mycobacteriol. Dep., Pasteur Inst. Iran, Pasteur Ave., Tehran 13164, Iran
SO Scandinavian Journal of Infectious Diseases, (1998) Vol. 30, No. 5, pp. 477-480. print.
CODEN: SJIDB7. ISSN: 0036-5548.

DT Article
LA English
ED Entered STN: 31 Mar 1999
Last Updated on STN: 31 Mar 1999
AB Two rapid procedures, restriction enzyme analysis of the amplified segment of the gene encoding for the 65000 mol. wt heat shock protein and a polymerase chain reaction with single universal ***primer*** (UP-PCR), were used for the ***identification*** of ***Mycobacterium*** tuberculosis complex (n = 47) and proving the species identity of non-tuberculous ***mycobacteria*** (NTM, n = 36) cultured from clinical samples by comparing the resulting DNA banding pattern with patterns derived from ***mycobacterial*** type strains (n = 24). UP-PCR assay provided a rather wide limit of tolerance for variations in procedure. Although ***mycobacterial*** strains were found to generate species-specific banding patterns in both assays, M. tuberculosis and M. bovis strains and isolates produced nearly the same DNA patterns, which were very distinctive from that of all NTM tested. Investigation of the majority of M. fortuitum (n = 14) and M. kansasii (n = 7), ***mycobacteria*** most frequently causing ***mycobacterioses*** in the region, as well as other NTM isolates, showed reproducible patterns characteristic of corresponding type strains. Both methods combine the advantages of ordinary PCR and PCR 'fingerprinting', namely, the species-specific DNA pattern and ***primers*** applicable to different species. They may be applied as rapid tests for proving the identity of ***Mycobacterium*** species in a clinical laboratory.
TI Use of restriction enzyme analysis of amplified DNA coding for the ***hsp65*** gene and polymerase chain reaction with universal ***primer*** for rapid differentiation of ***Mycobacterium*** species in the clinical laboratory.
AB. . . of the gene encoding for the 65000 mol. wt heat shock protein and a polymerase chain reaction with single universal ***primer*** (UP-PCR), were used for the ***identification*** of ***Mycobacterium*** tuberculosis complex (n = 47) and proving the species identity of non-tuberculous ***mycobacteria*** (NTM, n = 36) cultured from clinical samples by comparing the resulting DNA banding pattern with patterns derived from ***mycobacterial*** type strains (n = 24). UP-PCR assay provided a rather wide limit of tolerance for variations in procedure. Although ***mycobacterial*** strains were found to generate species-specific banding patterns in both assays, M. tuberculosis and M. bovis strains and isolates produced. . . of all NTM tested. Investigation of the majority of M. fortuitum (n = 14) and M. kansasii (n = 7), ***mycobacteria*** most frequently causing ***mycobacterioses*** in the region, as well as other NTM isolates, showed reproducible patterns characteristic of corresponding type strains. Both methods combine the advantages of ordinary PCR and PCR 'fingerprinting', namely, the species-specific DNA pattern and ***primers*** applicable to different species. They may be applied as rapid tests for proving the identity of ***Mycobacterium*** species in a clinical laboratory.
IT . . . Concepts
Clinical Chemistry (Allied Medical Sciences); Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA: analysis, bacterial; ***Mycobacterium*** ***hsp65*** gene
IT Methods & Equipment
polymerase chain reaction: DNA amplification, bacteria ***identification*** method, molecular genetic method,

diagnostic method, sequencing techniques, analytical method; restriction enzyme analysis: analytical method, bacteria
identification method, ***diagnostic*** method, molecular genetic method
ORGN . . .
Taxa
Primates; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
human: patient
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium bovis: pathogen
Mycobacterium fortuitum: pathogen
Mycobacterium spp.: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 14 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1992:391344 BIOSIS <<LOGINID::20090617>>
DN PREV199294063519; BA94:63519
TI DIFFERENTIATION OF SLOWLY GROWING ***MYCOBACTERIUM*** -SPP INCLUDING ***MYCOBACTERIUM*** -TUBERCULOSIS BY GENE AMPLIFICATION AND RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS.
AU PLIKAYTIS B B [Reprint author]; PLIKAYTIS B D; YAKRUS M A; BUTLER W R; WOODLEY C L; SILCOX V A; SHINNICK T M
CS DIVISION BACTERIAL MYCOTIC DISEASES, NATIONAL CENTER INFECTIOUS DISEASES, CENTERS DISEASE CONTROL, ATLANTA, GA 30333, USA
SO Journal of Clinical Microbiology, (1992) Vol. 30, No. 7, pp. 1815-1822. CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 24 Aug 1992
Last Updated on STN: 24 Aug 1992
AB A two-step assay combining a gene amplification step and a restriction fragment length polymorphism analysis was developed to differentiate the ***Mycobacterium*** species that account for > 90% of potentially pathogenic isolates and >86% of all isolates in clinical laboratories in the United States. These species are M. tuberculosis, M. bovis, M. avium, M. intracellulare, M. kansasii, and M. gordonae. With lysates of pure cultures as the template, two oligonucleotide ***primers*** that amplified an .apprx.1,380-bp portion of the ***hsp65*** gene from all 139 strains of 19 ***Mycobacterium*** species tested, but not from the 19 non- ***Mycobacterium*** species tested, were ***identified*** . Digestion of the amplicons from 126 strains of the six most commonly isolated ***Mycobacterium*** species with the restriction enzymes BstNI and XhoI in separate reactions generated restriction fragment patterns that were distinctive for each of these species, except for those of M. tuberculosis and M. bovis, which were not distinguishable. By including size standards in each sample, the restriction fragment profiles

could be normalized to a fixed distance and the similarities of patterns could be calculated by using a computer-aided comparison program. The availability of this data base should enable the ***identification*** of an unknown ***Mycobacterium*** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base of known patterns.

TI DIFFERENTIATION OF SLOWLY GROWING ***MYCOBACTERIUM*** -SPP INCLUDING ***MYCOBACTERIUM*** -TUBERCULOSIS BY GENE AMPLIFICATION AND RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS.

AB. . . A two-step assay combining a gene amplification step and a restriction fragment length polymorphism analysis was developed to differentiate the ***Mycobacterium*** species that account for > 90% of potentially pathogenic isolates and >86% of all isolates in clinical laboratories in the. . . bovis, M. avium, M. intracellulare, M. kansasii, and M. gordonae. With lysates of pure cultures as the template, two oligonucleotide ***primers*** that amplified an .apprx.1,380-bp portion of the ***hsp65*** gene from all 139 strains of 19 ***Mycobacterium*** species tested, but not from the 19 non-***Mycobacterium*** species tested, were ***identified*** . Digestion of the amplicons from 126 strains of the six most commonly isolated ***Mycobacterium*** species with the restriction enzymes BstNI and XhoI in separate reactions generated restriction fragment patterns that were distinctive for each. . . of patterns could be calculated by using a computer-aided comparison program. The availability of this data base should enable the ***identification*** of an unknown ***Mycobacterium*** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base. . .

IT Miscellaneous Descriptors
MYCOBACTERIUM -BOVIS ***MYCOBACTERIUM*** -AVIUM ***MYCOBACTERIUM*** -INTRACELLULARE ***MYCOBACTERIUM*** -KANSASII ***MYCOBACTERIUM*** -GORDONAE MOLECULAR ***DIAGNOSTIC*** METHOD COMPUTER AIDED COMPARISON

ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 15 OF 71 CABA COPYRIGHT 2009 CABI on STN
AN 2008:76969 CABA <<LOGINID::20090617>>
DN 20083066496
TI Molecular characterization of a novel fastidious ***mycobacterium*** causing lepromatous lesions of the skin, subcutis, cornea, and conjunctiva of cats living in Victoria, Australia
AU Fyfe, J. A.; McCowan, C.; O'Brien, C. R.; Globan, M.; Birch, C.; Revill, P.; Barrs, V. R. D.; Wayne, J.; Hughes, M. S.; Holloway, S.; Malik, R.
CS Victorian Infectious Diseases Reference Laboratory, 10 Wreckyn St., North Melbourne, Victoria 3051, Australia. janet.fyfe@mh.org.au
SO Journal of Clinical Microbiology, (2008) Vol. 46, No. 2, pp. 618-626. 27 ref.
Publisher: American Society for Microbiology (ASM). Washington
ISSN: 0095-1137
URL: http://jcm.asm.org/
CY United States
DT Journal

LA English
ED Entered STN: 4 Apr 2008
Last Updated on STN: 4 Apr 2008
AB Between 1999 and 2006, 15 cats were ***diagnosed*** with disease attributable to a novel ***mycobacterial*** species. The infections consisted of granulomatous lesions in the skin, subcutis, and ocular or periocular tissues with an indolent but progressive clinical course. Lesions typically were found in facial regions or on the distal limbs. Cats of all ages and both sexes were affected. Infections often were challenging to treat, although they could be cured using surgery in concert with combination antimicrobial therapy. Microscopically, lesions were granulomatous to pyogranulomatous and contained numerous acid-fast bacilli. Scanty cultures of the causal microorganisms occasionally could be obtained in ***mycobacterial*** broth, but subculture to solid media failed. When cultures were not available, DNA was extracted from fresh tissue, lyophilized material, and formalin-fixed, paraffin-embedded tissues from lesions. PCR amplification of the 5[prime] end of the 16S rRNA gene and regions within four additional loci (ITS1, ***hsp65*** , rpoB, and sodA) was performed with various efficiencies using ***mycobacterial*** ***primers*** . Nucleotide sequences were unique for each locus tested. Nucleotide sequences obtained from individual cases were identical for each locus for which the amplification was successful. Phylogenetic analysis performed using concatenated partial 16S rRNA and ***hsp65*** gene sequences indicated that this novel ***mycobacterial*** species from Victoria is a member of the ***Mycobacterium*** simiae-related group, taxonomically related to the ***mycobacterium*** causing leproid granulomas in dogs throughout the world. Based on the clustering of cases, we refer to this novel species as ***Mycobacterium*** sp. strain Tarwin.
TI Molecular characterization of a novel fastidious ***mycobacterium*** causing lepromatous lesions of the skin, subcutis, cornea, and conjunctiva of cats living in Victoria, Australia.
AB Between 1999 and 2006, 15 cats were ***diagnosed*** with disease attributable to a novel ***mycobacterial*** species. The infections consisted of granulomatous lesions in the skin, subcutis, and ocular or periocular tissues with an indolent but. . . were granulomatous to pyogranulomatous and contained numerous acid-fast bacilli. Scanty cultures of the causal microorganisms occasionally could be obtained in ***mycobacterial*** broth, but subculture to solid media failed. When cultures were not available, DNA was extracted from fresh tissue, lyophilized material,. . . from lesions. PCR amplification of the 5[prime] end of the 16S rRNA gene and regions within four additional loci (ITS1, ***hsp65*** , rpoB, and sodA) was performed with various efficiencies using ***mycobacterial*** ***primers*** . Nucleotide sequences were unique for each locus tested. Nucleotide sequences obtained from individual cases were identical for each locus for which the amplification was successful. Phylogenetic analysis performed using concatenated partial 16S rRNA and ***hsp65*** gene sequences indicated that this novel ***mycobacterial*** species from Victoria is a member of the ***Mycobacterium*** simiae-related group, taxonomically related to the ***mycobacterium*** causing leproid granulomas in dogs throughout the world. Based on the clustering of cases, we refer to this novel species as ***Mycobacterium*** sp. strain Tarwin.
BT. . . Australasia; Oceania; Developed Countries; Commonwealth of Nations; OECD Countries; Felis; Felidae; Fissipeda; carnivores; mammals; vertebrates; Chordata; animals; small mammals; eukaryotes; ***Mycobacteriaceae*** ; Firmicutes; bacteria; prokaryotes;

Mycobacterium ; Australia
ST bacterial infections; bacterioses; clinical picture; ***Mycobacterium*** simiae; rRNA
ORGN cats; ***Mycobacterium***

L9 ANSWER 16 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2009:601805 CAPLUS <<LOGINID::20090617>>
TI Cloning and sequence analysis of ***Mycobacterium*** paratuberculosis ***hsp65*** gene
AU Xu, Feng-yu; Hu, Yu-qing; Zeng, Fan-li; Jiang, Xiu-yun; He, Zhao-yang
CS College of Animal Science and Technology, Jilin Agricultural University, Changchun, 130118, Peop. Rep. China
SO Jilin Nongye Daxue Xuebao (2009), 31(2), 204-207
CODEN: JNDXE8; ISSN: 1000-5684
PB Jilin Nongye Daxue Xuebao Bianjibu
DT Journal
LA Chinese
AB The genomic DNA was extd. from ***Mycobacterium*** paratuberculosis(MP) strain C - 2. The secreted protein ***hsp65*** gene was amplified with a pair of specific ***primers*** using polymerase chain reaction (PCR). PCR product was anapproximate 1 626 bp DNA segment. The clone vector pGEM-T- ***hsp65*** was constructed successfully by the PCR product that was cloned into pGEM-T vector using T - A clone technique, and the recombinant clone was ***identified*** by using complementation test, plasmid size test, restrictional enzyme assay, plasmid PCR ***identification*** and recombinant plasmid sequence anal. The anal. indicated that the ***hsp65*** gene was very conservative in MP. These results could serve as a basis for further study on the usefulness of ***hsp65*** gene and immunogenicity characteristic of ***hsp65*** gene expression product.
TI Cloning and sequence analysis of ***Mycobacterium*** paratuberculosis ***hsp65*** gene
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L9 ANSWER 17 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:1297669 CAPLUS <<LOGINID::20090617>>
DN 149:508418
TI Immunological capture and PCR detection of ***Mycobacteria*** from environmental samples
IN Kluge, Christoph; Gutierrez Perez, Maria-Cristina; Marchal, Gilles
PA Institut Pasteur, Fr.; Centre d'Analyses Environnementales (CAE)
SO Can. Pat. Appl., 68pp.
CODEN: CPXXEB
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CA 2629465	A1	20081019	CA 2008-2629465	20080418
	CA 2585670	A1	20081019	CA 2007-2585670	20070419
	CA 2618289	A1	20081019	CA 2008-2618289	20080121
	WO 2008129419	A2	20081030	WO 2008-IB1255	20080421
	WO 2008129419	A3	20090430		

W: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AP, EA, EP, OA

PRAI	CA 2007-2585670	A	20070419
	CA 2008-2618289	A	20080121

AB Methods of detecting and isolating ***Mycobacteria*** from the environment are described. The method can be applied to non-tuberculosis ***Mycobacteria*** that may pose a health risk to the elderly and immunocompromised. The ***Mycobacteria*** are selectively captured using antibodies immobilized on magnetic particles. They can then be quantified by PCR of a marker gene such as sodA. Use of polyclonal antibodies is demonstrated. The method can detect 100 cfu of ***Mycobacterium*** in six hours.

TI Immunological capture and PCR detection of ***Mycobacteria*** from environmental samples

AB Methods of detecting and isolating ***Mycobacteria*** from the environment are described. The method can be applied to non-tuberculosis ***Mycobacteria*** that may pose a health risk to the elderly and immunocompromised. The ***Mycobacteria*** are selectively captured using antibodies immobilized on magnetic particles. They can then be quantified by PCR of a marker gene such as sodA. Use of polyclonal antibodies is demonstrated. The method can detect 100 cfu of ***Mycobacterium*** in six hours.

ST ***Mycobacterium*** detection immobilized antibody PCR

IT Cell wall
(***Mycobacterium*** , antibodies to; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Oryctolagus cuniculus
Rabbit
(anti-***Mycobacterium*** antibodies from; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Magnetic particles
(anti-***Mycobacterium*** antibodies immobilized on; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Biofilms (microbial)
Drinking waters
Environmental analysis
Milk
Sputum

Waters
(detection of ***Mycobacterium*** in; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Food analysis
(detection of non-tuberculosis ***Mycobacterium*** in; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT ***Mycobacterium*** BCG
Mycobacterium abscessus
Mycobacterium avium
Mycobacterium gordonae
Mycobacterium kansasii
Mycobacterium xenopi
(detection of; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Enzyme-linked immunosorbent assay
Immunoassay
(for ***Mycobacterium*** ; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for detection of ***Mycobacterium*** ; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(gyrA, as marker in detection of ***Mycobacterium*** by PCR; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(***hsp65*** , as marker in detection of ***Mycobacterium*** by PCR; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(immobilized, to ***Mycobacterium*** ; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT ***Mycobacterium***
(immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(inhA, as marker in detection of ***Mycobacterium*** by PCR; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT ***Diagnosis***
(mol., of non-tuberculosis ***Mycobacterial*** infection; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Bacterial infection
(non-tuberculosis ***Mycobacterium*** , ***diagnosis*** of; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Polymerase chain reaction
(quant., for detection of ***Mycobacterium*** ; immunol. capture and

PCR detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(sodA, as marker in detection of ***Mycobacterium*** by PCR; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT 1072990-26-1 1072990-27-2 1072990-28-3 1072990-29-4 1072990-30-7 1072990-31-8 1072990-32-9 1072990-33-0 1072990-34-1 1072990-35-2 1072990-36-3 1072990-37-4
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** for detection of ***Mycobacterium*** ; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

L9 ANSWER 18 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:1230479 CAPLUS <<LOGINID::20090617>>
TI Detection and characterization of nocardia from patients ***diagnosed*** as tuberculosis in Egypt
AU Helal, Zeinab H.; Khan, Mazhar I.; El-Din Ashour, Mohamed Seif; Eissa, Somaia A.
CS Department of Microbiology and Immunology, Faculty of Pharmacy, Al-Azhar University, Cairo, Egypt
SO International Journal of Biomedical Science (Monterey Park, CA, United States) (2008), 4(3), 179-184
CODEN: IJBSDB; ISSN: 1550-9702
PB Master Publishing Group
DT Journal
LA English
AB Pulmonary tuberculosis and pulmonary nocardiosis are similar in most clin. symptoms and radiol. manifestation. In the developing countries like Egypt where tuberculosis is very common, anti-tuberculosis drugs are started on basis of radiol. and clin. symptoms. This study included 600 sputum specimens collected from 200 patients ***diagnosed*** as pulmonary tuberculosis from three chest hospitals in Egypt. IS6110 specific ***primer*** were selected for PCR to ***identify*** the ***Mycobacterium*** tuberculosis and ***hsp65*** gene specific ***primers*** were used for PCR and sequencing for the ***identification*** of ***Mycobacterium*** and Nocardial species. The region of the gene coding for 16S rRNA in Nocardia species were selected as genus specific ***primer*** sequences for a PCR and Real Time PCR assays. Our result confirmed that four whole DNA samples, extd. from sputum specimen from the pulmonary tuberculosis patients on anti-tuberculosis treatment, were Nocardia species. Three of them matched (99% homol.) with Nocardia farcinica (formerly Nocardia asteroid type V) and one match (83% homol.) with Nocardia pneumonia. Mol. methods such as PCR and real-time PCR for ***identification*** of Nocardia are rapid and accurate methods. No cross-reactions were obsd. using Real Time PCR specific for Nocordia with other closely related genera.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Detection and characterization of nocardia from patients ***diagnosed*** as tuberculosis in Egypt
AB . . . drugs are started on basis of radiol. and clin. symptoms. This study included 600 sputum specimens collected from 200 patients ***diagnosed*** as pulmonary tuberculosis from three chest hospitals in Egypt. IS6110 specific ***primer*** were selected for PCR to

identify the ***Mycobacterium*** tuberculosis and ***hsp65*** gene specific ***primers*** were used for PCR and sequencing for the ***identification*** of ***Mycobacterium*** and Nocardial species. The region of the gene coding for 16S rRNA in Nocardia species were selected as genus specific ***primer*** sequences for a PCR and Real Time PCR assays. Our result confirmed that four whole DNA samples, extd. from sputum. . . asteroid type V) and one match (83% homol.) with Nocardia pneumonia. Mol. methods such as PCR and real-time PCR for ***identification*** of Nocardia are rapid and accurate methods. No cross-reactions were obsd. using Real Time PCR specific for Nocordia with other. . .

ST Nocardia ***Mycobacterium*** pulmonary tuberculosis

IT INDEXING IN PROGRESS

IT INDEXING IN PROGRESS

IT rRNA

(16 S; detection and characterization of Nocardia from patients ***diagnosed*** as tuberculosis in Egypt)

IT Human

Mycobacterium tuberculosis

Tuberculosis

(detection and characterization of Nocardia from patients ***diagnosed*** as tuberculosis in Egypt)

L9 ANSWER 19 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2008:962412 CAPLUS <<LOGINID::20090617>>

DN 150:275953

TI A single-step sequencing method for the ***identification*** of ***Mycobacterium*** tuberculosis complex species

AU Djelouadji, Zoheira; Raoult, Didier; Daffe, Mamadou; Drancourt, Michel

CS Unite des Rickettsies CNRS UMR6020, IFR 48, Faculte de Medecine, Universite de la Mediterranee, Marseille, Fr.

SO PLoS Neglected Tropical Diseases (2008), 2(6), No pp. given
CODEN: PNTDAM; ISSN: 1935-2735
URL: http://www.plosntds.org/article/info%3Adoi%2F10.1371%2Fjournal.pntd.0000253

PB Public Library of Science

DT Journal; (online computer file)

LA English

AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely related species responsible for strictly human and zoonotic tuberculosis. Accurate species detn. is useful for the ***identification*** of outbreaks and epidemiol. links. ***Mycobacterium*** africanum and ***Mycobacterium*** canettii are typically restricted to Africa and M. bovis is a re-emerging pathogen. ***Identification*** of these species is difficult and expensive. The Exact Tandem Repeat D (ETR-D; alias ***Mycobacterial*** Interspersed Repetitive Unit 4) was sequenced in MTC species type strains and 110 clin. isolates, in parallel to ref. polyphasic ***identification*** based on phenotype profiling and sequencing of pncA, oxyR, ***hsp65*** , gyrB genes and the major polymorphism tandem repeat. Inclusion of M. tuberculosis isolates in the expanding, antibiotic-resistant Beijing clone was detd. by Rv0927c gene sequencing. The ETR-D (780-bp) sequence unambiguously ***identified*** MTC species type strain except M. pinnipedii and M. microti due to six single nucleotide polymorphisms, variable nos. (1-7 copies) of the tandem repeat and two deletions/insertions. The ETR-D sequencing agreed with phenotypic ***identification*** in 107/110 clin. isolates and with ref. polyphasic mol. ***identification*** in all isolates, comprising

98 M. tuberculosis, 5 M. bovis BCG type, 5 M. canettii, and 2 M. africanum. For M. tuberculosis isolates, the ETR-D sequence was not significantly assocd. with the Beijing clone. ETR-D sequencing allowed accurate, single-step ***identification*** of the MTC at the species level. It circumvented the current expensive, time-consuming polyphasic approach. It could be used to depict epidemiol. of zoonotic and human tuberculosis, esp. in African countries where several MTC species are emerging.

RE.CNT 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A single-step sequencing method for the ***identification*** of ***Mycobacterium*** tuberculosis complex species

AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely related species responsible for strictly human and zoonotic tuberculosis. Accurate species detn. is useful for the ***identification*** of outbreaks and epidemiol. links. ***Mycobacterium*** africanum and ***Mycobacterium*** canettii are typically restricted to Africa and M. bovis is a re-emerging pathogen. ***Identification*** of these species is difficult and expensive. The Exact Tandem Repeat D (ETR-D; alias ***Mycobacterial*** Interspersed Repetitive Unit 4) was sequenced in MTC species type strains and 110 clin. isolates, in parallel to ref. polyphasic ***identification*** based on phenotype profiling and sequencing of pncA, oxyR, ***hsp65*** , gyrB genes and the major polymorphism tandem repeat. Inclusion of M. tuberculosis isolates in the expanding, antibiotic-resistant Beijing clone was detd. by Rv0927c gene sequencing. The ETR-D (780-bp) sequence unambiguously ***identified*** MTC species type strain except M. pinnipedii and M. microti due to six single nucleotide polymorphisms, variable nos. (1-7 copies) of the tandem repeat and two deletions/insertions. The ETR-D sequencing agreed with phenotypic ***identification*** in 107/110 clin. isolates and with ref. polyphasic mol. ***identification*** in all isolates, comprising 98 M. tuberculosis, 5 M. bovis BCG type, 5 M. canettii, and 2 M. africanum. For M. tuberculosis isolates, the ETR-D sequence was not significantly assocd. with the Beijing clone. ETR-D sequencing allowed accurate, single-step ***identification*** of the MTC at the species level. It circumvented the current expensive, time-consuming polyphasic approach. It could be used to. . .

ST PCR exact tandem repeat D ***Mycobacterium*** species ***identification*** ; DNA sequence Senx3 Regx3 intergenic spacer ETRD repeat ***Mycobacterium*** ; sequence DNA gene oxyR ***hsp65*** ***Mycobacterium*** ; ***primer*** PCR DNA repeat ETRD ***Mycobacterium*** species ***identification***

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Cell morphology
Phenotypes
(ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT ***Mycobacterium*** tuberculosis

Polymerase chain reaction
(ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HSP 65; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Genetic element
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IGS (intergenic spacer), ETR-D repeat located in Senx3-Regx3 spacer region; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Genetic polymorphism
(INDEL; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(OxyR; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Regx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Senx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene Regx3, sensory transduction protein, sequence homolog; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene mptR; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic

use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gyrB; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT ***Diagnosis***
(mol.; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(mptR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(oxyR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA sequences
Mycobacterium BCG
Mycobacterium africanum
Mycobacterium bovis
Mycobacterium canettii
Mycobacterium caprae
Mycobacterium microti
Mycobacterium pinnipedii

Protein sequences
(partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Single nucleotide polymorphism
(partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(pncA; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65*** , gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; ETR-D sequencing for single-step

identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Repetitive DNA
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(tandem, exact D, ETR-D in Senx3-Regx3 intergenic spacer; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT Repetitive DNA
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(tandem; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT 1124387-63-8 1124387-64-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ETR-D-specific ***primer*** ; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

IT 1123333-08-3 1123333-09-4 1123333-11-8 1123333-12-9 1123333-14-1 1123333-15-2 1123333-17-4 1123333-18-5 1123333-20-9 1123333-21-0 1123333-23-2 1123333-24-3 1123333-26-5 1123333-27-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT 1088759-76-5 1088759-78-7 1088759-80-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

IT 420839-67-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene Senx3, sequence homolog; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT 1123333-07-2 1123333-10-7 1123333-13-0 1123333-16-3 1123333-19-6 1123333-22-1 1123333-25-4
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT 1088759-75-4 1088759-77-6 1088759-79-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

L9 ANSWER 20 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:455470 CAPLUS <<LOGINID::20090617>>
DN 149:324704
TI Construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis
AU Li, Yan; Deng, Junxia; Guan, Dawei
CS Department of EMT Center, The Affiliated Provincial Hospital, Anhui Medical University, Hefei, Anhui Province, 231000, Peop. Rep. China
SO Xinxiang Yixueyuan Xuebao (2007), 24(1), 29-33
CODEN: XYIXEQ; ISSN: 1004-7239
PB Xinxiang Yixueyuan Xuebao Bianji Weiyuanhui
DT Journal
LA Chinese
AB The eukaryotic expression vector based on ***HSP65*** gene of ***mycobacterium*** tuberculosis was constructed. ***HSP65*** gene was cloned from genome of ***mycobacterium*** tuberculosis H37Rv strain by PCR, and inserted into multiple cloning site A's corresponding sites of dicistronic eukaryotic expression vector pIRES to construct eukaryotic expression vector pIHSP65, then transfected into Hela cell by using poly-cation. Finally, the expression of ***HSP65*** protein was detected by immunochem. staining. The length and sequence of the cloned ***HSP65*** segment were correct. The pos. expression of ***HSP65*** in Hela cell, which had been transfection with recombinant plasmid, was ***identified*** by immunohistochem. method. The successful construction of eukaryotic expression vector pIHSP65 and effective expression in Hela cells, lays the foundation for constructing two-antigens dicistronic eukaryotic expression plasmid and further study in animal.
TI Construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis
AB The eukaryotic expression vector based on ***HSP65*** gene of ***mycobacterium*** tuberculosis was constructed. ***HSP65*** gene was cloned from genome of ***mycobacterium*** tuberculosis H37Rv strain by PCR, and inserted into multiple cloning site A's corresponding sites of dicistronic eukaryotic expression vector pIRES to construct eukaryotic expression vector pIHSP65, then transfected into Hela cell by using poly-cation. Finally, the expression of ***HSP65*** protein was detected by immunochem. staining. The length and sequence of the cloned ***HSP65*** segment were correct. The pos. expression of ***HSP65*** in Hela cell, which had been transfection with recombinant plasmid, was ***identified*** by immunohistochem. method. The successful construction of eukaryotic expression vector pIHSP65 and effective expression in Hela cells, lays the foundation. . .
ST cloning vaccine pIHSP65 ***Mycobacterium*** tuberculosis
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP65*** ; construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis)
IT Antibacterial agents
HeLa cell
Molecular cloning

Mycobacterium tuberculosis
Transformation, genetic
Vaccines
(construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis)
IT ***Primers*** (nucleic acid)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis)
IT Plasmid vectors
(pIHSP65; construction and expression of eukaryotic expression vector pIHSP65 of ***Mycobacterium*** tuberculosis)

L9 ANSWER 21 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:137939 CAPLUS <<LOGINID::20090617>>
DN 148:300601
TI PCR-RFLP analysis (PRA) of non tuberculous ***mycobacteria*** (NTM) isolated from animal specimens and environment using ***hsp65*** and rpoB genes
AU Bannalikar, A. S.; Verma, Rishendra
CS Indian Veterinary Research Institute, Uttar Pradesh, 243 122, India
SO Indian Journal of Animal Sciences (2007), 77(12), 1211-1218
CODEN: IJLAA4; ISSN: 0367-8318
PB Indian Council of Agricultural Research
DT Journal
LA English
AB Non tuberculous ***mycobacteria*** (99) comprising 34 isolates from animal specimens, 57 soil and 8 water samples from animal dwellings were ***identified*** on the basis of growth rate, pigmentation, colony morphol. and biochem. reactions. Of the 8 species recovered from animal specimens 4 (M. fortuitum, M. smegmatis, M. chelonae and M. abscessus) were prevalent in soil while only 2 of these species (M. fortuitum and M. smegmatis) prevailed in water samples. These isolates along with 13 ref. strains of ***mycobacteria*** were subjected to polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** and rpoB genes. All the isolates generated products of 439 bp and 360 bp in PCR of ***hsp65*** and rpoB genes resp. Restriction digestion of the product of ***hsp65*** and BstEII and HaeIII and that of rpoB with MspI and HaeIII in sep. reactions and anal. of digests by agarose gel electrophoresis revealed RFLP patterns characteristic for most of the species tested. Out of the 16- ***mycobacterial*** species evaluated, 13 produced a single PRA pattern, while 3 species generated 2 patterns in both the PRA methods. M. abscessus and M. chelonae were distinguishable from each other. M. fortuitum isolates were differentiated into M. fortuitum I and M. fortuitum II, M. avium complex isolates into M. intracellulare and M. avium, M. kansasii isolates into M. kansasii I and M. kansasii V and M. gordonae into M. gordonae II and M. gordonae (new type) by both the methods. Both the PRA methods could not make a distinction between M. tuberculosis and M. bovis however, PRA with ***hsp65*** was found better since it yielded relatively large sized and
distinct band.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI PCR-RFLP analysis (PRA) of non tuberculous ***mycobacteria*** (NTM) isolated from animal specimens and environment using ***hsp65*** and rpoB genes

AB Non tuberculous ***mycobacteria*** (99) comprising 34 isolates from animal specimens, 57 soil and 8 water samples from animal dwellings were ***identified*** on the basis of growth rate, pigmentation, colony morphol. and biochem. reactions. Of the 8 species recovered from animal specimens. . . of these species (M. fortuitum and M. smegmatis) prevailed in water samples. These isolates along with 13 ref. strains of ***mycobacteria*** were subjected to polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** and rpoB genes. All the isolates generated products of 439 bp and 360 bp in PCR of ***hsp65*** and rpoB genes resp. Restriction digestion of the product of ***hsp65*** and BstEII and HaeIII and that of rpoB with MspI and HaeIII in sep. reactions and anal. of digests by agarose gel electrophoresis revealed RFLP patterns characteristic for most of the species tested. Out of the 16- ***mycobacterial*** species evaluated, 13 produced a single PRA pattern, while 3 species generated 2 patterns in both the PRA methods. M.. . . the methods. Both the PRA methods could not make a distinction between M. tuberculosis and M. bovis however, PRA with ***hsp65*** was found better since it yielded relatively large sized and distinct band.

ST PCR RFLP gene ***hsp65*** nontuberculous ***mycobacteria*** detection discrimination; gene rpoB PCR RFLP nontuberculous ***mycobacteria*** detection discrimination; ***Mycobacterium*** prevalence water soil animal tissue PCR RFLP

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT ***Mycobacterium*** avium
(complex; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Animal tissue
Animalia
Animals
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium fortuitum
Mycobacterium gordonae
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium smegmatis
Polymerase chain reaction
Restriction fragment length polymorphism
Soils
(***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT DNA

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rpoB; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT 7732-18-5, Water, analysis
RL: AMX (Analytical matrix); ANST (Analytical study)
(***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

L9 ANSWER 22 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:1057364 CAPLUS <<LOGINID::20090617>>
DN 147:337125
TI Method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence
IN Kim, Bum Joon; Kim, Hyun Joo; Park, Hae Joon
PA Seoul National University Industry Foundation, S. Korea
SO Repub. Korea, No pp. given
CODEN: KRXXFC
DT Patent
LA Korean
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		

AB A method for ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of ***Mycobacterial*** species using a ***primer*** specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to ***identify*** non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C,
600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of ***primer*** pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous

mycobacteria and ***Mycobacterium*** tuberculosis comprises a ***primer*** pairs, and the sequences of the ***primers*** have been presented.

TI Method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence

AB A method for ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the. . . consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of ***Mycobacterial*** species using a ***primer*** specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to ***identify*** non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of ***primer*** pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis comprises a ***primer*** pairs, and the sequences of the ***primers*** have been presented.

ST ***Mycobacterium*** tuberculosis nontuberculous genotyping PCR ***Hsp65*** gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65; method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT Genotypes
Genotyping (method)
Mycobacterium
Mycobacterium tuberculosis
Polymerase chain reaction
Tuberculosis
(method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence)

L9 ANSWER 23 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:747037 CAPLUS <<LOGINID::20090617>>
DN 148:4726
TI Molecular ***identification*** by random amplified polymorphic DNA analysis of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clinical samples
AU Ortiz, Alberto; Esteban, Jaime; Zamora, Nieves
CS Department of Clinical Microbiology, Fundacion Jimenez Diaz-UTE, Madrid, 28040, Spain
SO Journal of Medical Microbiology (2007), 56(6), 871-872
CODEN: JMMIAV; ISSN: 0022-2615
PB Society for General Microbiology
DT Journal
LA English
AB A pseudo-outbreak of ***Mycobacterium*** fortuitum, probably due to cross-contamination from a true pos. urine specimen, detected in the lab. is described. All specimens sent to the ***mycobacteriol*** . lab. were decontaminated with N-acetylcysteine-NaOH according to commonly accepted protocols. After decontamination, all samples were inoculated into MGIT liq. culture medium (BD) and onto Coletsos and Lowenstein-Jensen slants (bioMsrieux). ***Identification*** of the isolates was performed using common biochem. tests and PCR-RFLP anal. of the ***hsp65*** gene. Susceptibility testing of the strains was done using amikacin, clarithromycin, ciprofloxacin and imipenem E-test strips on Muller-Hinton agar plates enriched with 5 % sheep blood incubated at 37.degree. in a 5% CO2 atmosphere for 3 days. The mol. epidemiol. anal. was done by the random amplified polymorphic DNA (RAPD) technique using the ***primers*** OPA-2, OPA-18, INS-2 and IS-986FP. Strains were considered to be identical when the electrophoretic pattern was the same with at least three ***primers*** . Other unrelated M. fortuitum strains isolated from clin. samples from our collection were used as controls. A NPRGM was recovered in five samples processed on the same day. During the inoculation in the culture media, samples were located near to each other, and even next to each other in some cases. In three samples, the ***mycobacterial*** strain was isolated in the MGIT medium, and in another one, only one colony grew on a Coletsos slant (bioMeritux).
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Molecular ***identification*** by random amplified polymorphic DNA analysis of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clinical samples
AB A pseudo-outbreak of ***Mycobacterium*** fortuitum, probably due to cross-contamination from a true pos. urine specimen, detected in the lab. is described. All specimens sent to the ***mycobacteriol*** . lab. were decontaminated with N-acetylcysteine-NaOH according to commonly accepted protocols. After decontamination, all samples were inoculated into MGIT liq. culture medium (BD) and onto Coletsos and Lowenstein-Jensen slants (bioMsrieux). ***Identification*** of the isolates was

performed using common biochem. tests and PCR-RFLP anal. of the ***hsp65*** gene. Susceptibility testing of the strains was done using amikacin, clarithromycin, ciprofloxacin and imipenem E-test strips on Muller-Hinton agar plates. . . atmosphere for 3 days. The mol. epidemiol. anal. was done by the random amplified polymorphic DNA (RAPD) technique using the ***primers*** OPA-2, OPA-18, INS-2 and IS-986FP. Strains were considered to be identical when the electrophoretic pattern was the same with at least three ***primers*** . Other unrelated M. fortuitum strains isolated from clin. samples from our collection were used as controls. A NPRGM was recovered. . . samples were located near to each other, and even next to each other in some cases. In three samples, the ***mycobacterial*** strain was isolated in the MGIT medium, and in another one, only one colony grew on a Coletsos slant (bioMeritux).

ST ***Mycobacterium*** phenotype antibiotic resistance RAPD

IT Antibiotic resistance
Human
Mycobacterium fortuitum
Phenotypes
RAPD analysis
(mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

IT Epidemiology
(mol.; mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

IT 37517-28-5, Amikacin 64221-86-9, Imipenem 81103-11-9, Clarithromycin 85721-33-1, Ciprofloxacin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

L9 ANSWER 24 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:673037 CAPLUS <<LOGINID::20090617>>
DN 147:90504
TI Method and kit for detecting the presence or absence of a target cell in a sample
IN Angles D'Auriac, Marc
PA Genpoint A/S, Norway; Gardner, Rebecca
SO PCT Int. Appl., 41pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2007068904	A1	20070621	WO 2006-GB4629	20061212

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW

PI RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

AU	2006324486	A1	20070621	AU 2006-324486	20061212
CA	2631877	A1	20070621	CA 2006-2631877	20061212
EP	1969138	A1	20080917	EP 2006-820489	20061212
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR				
JP	2009518053	T	20090507	JP 2008-545076	20061212
CN	101374960	A	20090225	CN 2006-80046310	20080610
PRAI GB	2005-25231	A	20051212		
WO	2006-GB4629	W	20061212		

AB The present invention relates to a method for detecting the presence or absence of a target cell in a sample, said method comprising (a) binding cells in said sample to a particulate and mixable solid support; (b) eluting the cells from the solid support without the use of competitor mols. to disrupt the interaction between the cell and the solid support; (c) after lysis of said cells, detecting the presence or absence of nucleic acid characteristic of said target cell, wherein said solid support does not have antibodies or antibody fragments immobilized thereon. Kits for carrying out the method of the invention are also provided. BUGS'n BEADS BW buffer and magnetic beads were added to urine samples and samples were mixed during incubation for 15 min. The beads were immobilized to the side of the tubes using a magnetic separator and the supernatant was removed. The beads were washed with 70% ethanol in water, incubated at 80.degree. for 10 min, and immobilized by magnetic sepn. Supernatant was analyzed by PCR amplification for Chlamydia trachomatis.

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

ST target cell detection binding particulate mixable solid; nucleic acid ***identification*** particulate sepd target cell; Chlamydia trachomatis
detection urine magnetic bead sepn PCR amplification

IT Bordetella pertussis
Chlamydia
Chlamydia pneumoniae
Chlamydia trachomatis
Gram-negative bacteria
Mollicutes
Mycobacterium abscessus
Mycoplasma pneumoniae
Neisseria gonorrhoeae
(as cell; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT Plasmids
(cryptic, PCR ***primers*** for detection of nucleic acid for, of Chlamydia trachomatis; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(***hsp65*** , PCR ***primers*** for detection of nucleic acid for, of ***Mycobacterium*** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-58-6 942319-59-7
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(as PCR ***primer*** in detection of human respiratory syncytial virus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-54-2
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(as forward PCR ***primer*** in detection of Chlamydia trachomatis in urine samples; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-56-4
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(as forward PCR ***primer*** in detection of ***Mycobacterium*** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-55-3
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(as reverse PCR ***primer*** in detection of Chlamydia trachomatis in urine samples; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-57-5
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(as reverse PCR ***primer*** in detection of ***Mycobacterium*** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

L9 ANSWER 25 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:1304935 CAPLUS <<LOGINID::20090617>>
DN 146:515458
TI Differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing
AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Bum-Joon
CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea
SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862

CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Here we describe a novel duplex PCR method which can differentiate ***Mycobacterium*** tuberculosis and nontuberculosis ***mycobacteria*** (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for ***identifying*** ***mycobacterial*** culture isolates at the species level.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing
AB Here we describe a novel duplex PCR method which can differentiate ***Mycobacterium*** tuberculosis and nontuberculosis ***mycobacteria*** (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin.. . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . . sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for ***identifying*** ***mycobacterial*** culture isolates at the species level.
ST ***Mycobacterium*** species differentiation ***hsp65*** duplex PCR restriction analysis sequencing
IT DNA sequence analysis
Mycobacterium tuberculosis
Tuberculosis
(differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)
IT Genetic methods
(duplex-PCR-based restriction anal.; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by
duplex-PCR-based restriction anal. and direct sequencing)
IT Polymerase chain reaction
(duplex; differentiation of ***mycobacterial*** species by

hsp65 duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT Human
(isolates from; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT ***Diagnosis***
(mol.; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT ***Mycobacterium***
(nontuberculosis; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal.
and direct sequencing)
IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5 936858-61-6 936858-62-7 936858-64-9 936858-65-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; differentiation of ***mycobacterial*** species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

L9 ANSWER 26 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:1013535 CAPLUS <<LOGINID::20090617>>
DN 146:39451
TI Genetic analysis of ***Mycobacterium*** avium complex strains used for producing purified protein derivatives
AU Semret, Makeda; Bakker, Douwe; Smart, Nonie; Olsen, Ingrid; Haslov, Kaare; Behr, Marcel A.
CS McGill University Health Centre, Montreal, QC, Can.
SO Clinical and Vaccine Immunology (2006), 13(9), 991-996
CODEN: CVILA6; ISSN: 1556-6811
PB American Society for Microbiology
DT Journal
LA English
AB For over a century, purified protein derivs. (PPD) have been used to detect ***mycobacterial*** infections in humans and livestock. Among these, reagents to detect infections by ***Mycobacterium*** avium complex organisms have been produced, but the utility of these reagents has not been clearly established due in part to limited biol. and immunol. standardization. Because there is little information about the strains used to produce these reagents (avian PPD, intracellulare PPD, scrofulaceum PPD, and Johnin), we have performed genetic characterizations of strains used to produce these products. Sequence anal. of 16S rRNA and the ***hsp65*** gene provided results concordant with species designations provided for M. avium, ***Mycobacterium***

intracellulare, and ***Mycobacterium*** scrofulaceum organisms. For M. avium strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase genomic deletion in certain Johnin-producing strains, in addn. to genomic variability inherent to the particular M. avium subspecies. Our findings indicate that considerable genomic differences exist between organisms used for reagents and the infecting organism being studied. These results serve as a baseline for potency studies of different prepns. and should aid in comparative studies of newly discovered antigens for the ***diagnosis*** of infection and disease by M. avium complex organisms.

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Genetic analysis of ***Mycobacterium*** avium complex strains used for producing purified protein derivatives

AB For over a century, purified protein derivs. (PPD) have been used to detect ***mycobacterial*** infections in humans and livestock. Among these, reagents to detect infections by ***Mycobacterium*** avium complex organisms have been produced, but the utility of these reagents has not been clearly established due in part. . . Johnin), we have performed genetic characterizations of strains used to produce these products. Sequence anal. of 16S rRNA and the ***hsp65*** gene provided results concordant with species designations provided for M. avium, ***Mycobacterium*** intracellulare, and ***Mycobacterium*** scrofulaceum organisms. For M. avium strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase. . . a baseline for potency studies of different prepns. and should aid in comparative studies of newly discovered antigens for the ***diagnosis*** of infection and disease by M. avium complex organisms.

ST multiplex PCR ***Mycobacterium*** genotyping purified protein deriv

IT rRNA
RL: ANT (Analyte); ANST (Analytical study)
(16 S; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Heat-shock proteins
RL: ANT (Analyte); ANST (Analytical study)
(HSP 65, gene ***hsp65*** ; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Genotyping (method)
Mycobacterium avium
Mycobacterium intracellulare
Mycobacterium scrofulaceum
(PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Mutation
(deletion, LSPin (large sequence polymorphism); PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified
protein derivs.)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(***hsp65*** ; PCR anal. of ***Mycobacterium*** avium complex

strains used for producing purified protein derivs.)
IT Microsatellite DNA
RL: ANT (Analyte); ANST (Analytical study)
(locus 1, locus 2, locus 8, locus 9; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)
IT Polymerase chain reaction
(multiplex; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)
IT Tuberculin
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(purified protein deriv.; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)
IT 916531-71-0 916531-72-1 916531-73-2 916531-74-3 916531-75-4
916531-76-5 916531-77-6 916531-78-7 916531-79-8 916531-80-1
916531-81-2 916531-82-3 916531-83-4 916531-84-5 916531-85-6
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** ; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

L9 ANSWER 27 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:996526 CAPLUS <<LOGINID::20090617>>
DN 145:466501
TI ***Primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain
IN Fan, Hong; Ying, Binwu; Wang, Lanlan; Wen, Fuqiang
PA West China Hospital, Sichuan University, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 21pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CN 1834258	A	20060920	CN 2005-10022138	20051125
	CN 100368559	C	20080213		
PRAI	CN 2005-10022138		20051125		

AB The invention provides a ***primer*** sets for detection of ***Mycobacterium*** tuberculosis. The method comprises: (1) adding non-bacterial genome sequences YB1 and YB2 to 5' end of oligonucleotide ***primer*** P1 and P2 resp. to obtain specific long ***primers*** YB1-P1 and YB2-P2 as ***primer*** pairs for the first stage PCR in multi-amplification process, and (2) using the YB1 and YB2 as ***primer*** pairs for the second stage PCR in multi-amplification process. The method provided in this invention can be used of ***identification*** of ***Mycobacterium*** tuberculosis different strain.
TI ***Primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain
AB The invention provides a ***primer*** sets for detection of ***Mycobacterium*** tuberculosis. The method comprises: (1) adding non-bacterial genome sequences YB1 and YB2 to 5' end of oligonucleotide ***primer*** P1 and P2 resp. to obtain specific long ***primers*** YB1-P1 and YB2-P2 as ***primer*** pairs for the first stage PCR in multi-amplification process, and (2) using the YB1 and YB2 as ***primer*** pairs for the second stage PCR in multi-amplification

process. The method provided in this invention can be used of ***identification*** of ***Mycobacterium*** tuberculosis different strain.

ST ***Mycobacterium*** tuberculosis strain PCR ***primer***

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(IS6110; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(for 32kDa protein, amplification of; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(for ***hsp65*** ; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(mtp40; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT Genetic methods
Mycobacterium tuberculosis
PCR (polymerase chain reaction)
(***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT ***Primers*** (nucleic acid)
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT 913582-98-6 913582-99-7
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

IT 913583-10-5, 1: PN: CN1834258 SEQID: 1 unclaimed DNA 913583-11-6, 2: PN: CN1834258 SEQID: 2 unclaimed DNA 913583-12-7, 3: PN: CN1834258 SEQID: 3 unclaimed DNA 913583-13-8, 4: PN: CN1834258 SEQID: 4 unclaimed DNA
913583-14-9 913583-15-0 913583-16-1 913583-17-2 913583-18-3
913583-19-4 913583-20-7 913583-21-8 913583-22-9 913583-23-0
913583-24-1 913583-25-2 913583-26-3 913583-27-4 913583-28-5
913583-29-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; ***primer*** designing for multiple PCR for detection of ***Mycobacterium*** tuberculosis strain)

L9 ANSWER 28 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:986878 CAPLUS <<LOGINID::20090617>>
DN 146:352092
TI Development of PCR-RFLP for ***identification*** of eight ***mycobacterial*** species
AU Li, Xiaojie; Wang, Hongsheng; Wu, Qinxue; Cui, Pangen; Liu, Xunquan
CS Institute of Dermatology, Chinese Academy of Medical Sciences and Peking Union Medical College, Nanjing, 210042, Peop. Rep. China
SO Zhonghua Pifuke Zazhi (2005), 38(9), 533-535

CODEN: CHFTAJ; ISSN: 0412-4030
PB Zhongguo Yixue Kexueyuan Pifubing Yanjiuso
DT Journal
LA Chinese
AB A PCR-RFLP method for the ***identification*** of eight ***mycobacterial*** species was developed. PCR was performed targeting the gene encoding 65-kDa heat shock protein which was common to all ***mycobacteria*** . Two restriction enzymes, BstE II and Hae III, were used to digest the PCR products, and specific restriction patterns of different ***mycobacteria*** were obtained. The specific restriction patterns of different ***mycobacteria*** were identical to the data previously reported. M. avium, M. intracellulare, M. kansasii, M. tuberculosis, M. scrofulaceum, M. marinum, M. fortuitum and M. chelonae could be differentiated in one expt. by PCR-RFLP.
TI Development of PCR-RFLP for ***identification*** of eight ***mycobacterial*** species
AB A PCR-RFLP method for the ***identification*** of eight ***mycobacterial*** species was developed. PCR was performed targeting the gene encoding 65-kDa heat shock protein which was common to all ***mycobacteria*** . Two restriction enzymes, BstE II and Hae III, were used to digest the PCR products, and specific restriction patterns of different ***mycobacteria*** were obtained. The specific restriction patterns of different ***mycobacteria*** were identical to the data previously reported. M. avium, M. intracellulare, M. kansasii, M. tuberculosis, M. scrofulaceum, M. marinum, M.. . .
ST ***Mycobacterium*** heat shock protein 65 PCR RFLP; PCR RFLP detection ***Mycobacterium*** heat shock protein ***hsp65*** gene
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65; PCR-RFLP for ***identification*** of ***Mycobacterial*** species)
IT ***Mycobacterium*** avium
Mycobacterium chelonae
Mycobacterium fortuitum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium marinum
Mycobacterium scrofulaceum
Mycobacterium tuberculosis
Polymerase chain reaction
Restriction fragment length polymorphism
(PCR-RFLP for ***identification*** of ***Mycobacterial*** species)
IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(***hsp65*** ; PCR-RFLP for ***identification*** of ***Mycobacterial*** species)
IT ***Diagnosis***
(mol.; PCR-RFLP for ***identification*** of ***Mycobacterial*** species)
IT 930134-85-3 930134-86-4
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; PCR-RFLP for ***identification*** of ***Mycobacterial*** species)
IT 81295-18-3 93229-61-9, Restriction endonuclease, BstE II

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR-RFLP for ***identification*** of ***Mycobacterial*** species)

L9 ANSWER 29 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:517462 CAPLUS <<LOGINID::20090617>>
DN 146:177739
TI Rapid detection and species ***identification*** of ***Mycobacterium*** spp. using real-time PCR and DNA-Microarray
AU Tobler, Nadia E.; Pfunder, Monika; Herzog, Katrin; Frey, Juerg E.; Altwegg, Martin
CS Institute of Medical Microbiology, University of Zurich, Zurich, CH-8028, Switz.
SO Journal of Microbiological Methods (2006), 66(1), 116-124
CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier B.V.
DT Journal
LA English
AB Infections with ***mycobacteria*** are an important issue in public health care. Here we present a proof-of-principle' concept for the ***identification*** of 37 different ***Mycobacterium*** species using 5' exonuclease real-time PCR and DNA microarray based on the region upstream of the 65 kDa heat shock protein. With our two PCR probes, one complementary to all ***mycobacteria*** species, the other specific for the M. tbc-complex, 34 species were properly classified by real-time PCR. After reamplification and hybridization to a DNA microarray, all species showed a specific pattern. All 10 blindly tested pos. cultures revealed a pos. real-time PCR signal with the genus probe. After reamplification and hybridization, six samples could unambiguously be ***identified*** . One sample showed a mixt. of presumably three species-specific patterns and sequencing the 16S rRNA confirmed the presence of a mixt. The hybridization results of three specimens could not be interpreted because the signal to background ratio was not sufficient. Two samples considered as neg. controls (LAL Reagent Water (Cambrex) and DNA of Candida albicans) gave neither a genus nor a M. tbc-complex pos. PCR signal. Based on these results we consider our method to be a promising tool for the rapid ***identification*** of different ***mycobacteria*** species, with the advantage of possible ***identification*** of mixed infections or contaminations.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Rapid detection and species ***identification*** of ***Mycobacterium*** spp. using real-time PCR and DNA-Microarray
AB Infections with ***mycobacteria*** are an important issue in public health care. Here we present a proof-of-principle' concept for the ***identification*** of 37 different ***Mycobacterium*** species using 5' exonuclease real-time PCR and DNA microarray based on the region upstream of the 65 kDa heat shock protein. With our two PCR probes, one complementary to all ***mycobacteria*** species, the other specific for the M. tbc-complex, 34 species were properly classified by real-time PCR. After reamplification and hybridization. . . cultures revealed a pos. real-time PCR signal with the genus probe. After reamplification and hybridization, six samples could unambiguously be ***identified*** . One sample showed a mixt. of presumably three species-specific patterns and sequencing the 16S rRNA confirmed the presence of a. . .

tbc-complex pos. PCR signal. Based on these results we consider our method to be a promising tool for the rapid ***identification*** of different ***mycobacteria*** species, with the advantage of possible ***identification*** of mixed infections or contaminations.

ST real time PCR DNA microarray ***HSP65*** ***Mycobacterium*** species ***identification*** ; ***Mycobacterium*** species ***identification*** detection ***primer*** probe ***HSP65***

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, 65kDaf2, 65KDar3 and 65kDar4; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65, gene for; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)

IT ***Mycobacterium***
(description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT DNA microarray technology
Mycobacterium tuberculosis
(description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence, including ***Mycobacterium*** tuberculosis)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for ***HSP65*** , upstream region; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled with FAM, Cy3, Dabcyl or BHQ2; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT ***Diagnosis***
(mol.; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence, including ***Mycobacterium*** tuberculosis)

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , 65kDaf2, 65KDar3 and 65kDar4; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species

based on upstream ***HSP65*** gene sequence)
IT Polymerase chain reaction
(real-time; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)
IT 919130-80-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65KDar3; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)
IT 919130-79-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65kDaf2; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)
IT 919130-81-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** 65kDar4; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)
IT 919130-82-8D, 5'-labeled with FAM and 3'-labeled with Dabcyl
919130-83-9D, 5'-labeled with Cy3 and 3'-labeled with BHQ-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)
IT 6268-49-1D, Dabcyl, oligonucleotide conjugate 76823-03-5D, FAM, oligonucleotide conjugate 146368-16-3D, Cy3, oligonucleotide conjugate 374591-96-5D, BHQ-2, oligonucleotide conjugate
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)

L9 ANSWER 30 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:450735 CAPLUS <<LOGINID::20090617>>
DN 145:466102
TI Detection of ***Mycobacterium*** avium & M. tuberculosis from human sputum cultures by PCR-RFLP analysis of ***hsp65*** gene & pncA PCR
AU Bannalikar, A. S.; Verma, Rishendra
CS Mycobacteria Laboratory, Division of Bacteriology & Mycology, Indian Veterinary Research Institute, Izatnagar, India
SO Indian Journal of Medical Research (2006), 123(2), 165-172
CODEN: IMIREV; ISSN: 0971-5916
PB Indian Council of Medical Research
DT Journal
LA English

AB Background & objectives: ***Identification*** of ***mycobacteria*** by conventional methods is slow, labour intensive and may at times fail to produce precise results. Mol. techniques developed in the recent past, overcome these disadvantages facilitating rapid ***identification*** of most species. We undertook this study to characterize ***mycobacteria*** isolated from sputa of human patients suspected to have tuberculosis by conventional methods and later, by polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** gene and pncA PCR. Methods: Twenty two ***mycobacteria*** isolated from 30 sputum samples were ***identified*** based on growth rate, pigmentation, cultural and biochem. properties and subjected to PRA of ***hsp65*** gene involving amplification of ***hsp65*** gene and digestion of the product with BstEII and HaeIII in sep. reactions and anal. of digests by 3 per cent agarose gel electrophoresis. The ***mycobacteria*** were simultaneously evaluated by M. tuberculosis-specific and M. bovis-specific pncA PCR assays in sep. reactions. Results: With the conventional biochem. tests, the 22 sputum culture isolates were ***identified*** as M. tuberculosis (19) and M. avium complex (MAC) (3). PCR of ***hsp65*** gene yielded 439 bp product in all the ***mycobacteria*** tested. The RFLP patterns of three MAC isolates with BstEII and HaeIII were identical to ref. M. avium strain with two fragments in each of the digest. M. intracellulare ref. strain showed a distinct pattern with 3 fragments each in both enzyme digests. The PRA of ***hsp65*** confirmed MAC isolates as M. avium. M. tuberculosis isolates including H37Rv and M. bovis strains could not be discriminated by PRA of ***hsp65*** . The two pncA PCR assays (M. bovis-specific and M. tuberculosis-specific) detected specifically the resp. organisms with an amplification product of 185 bp. The MAC strains yielded no amplification product in both the pncA PCR assays. Interpretation & conclusion: PRA profiles of ***hsp65*** could differentiate MAC isolates into M. avium and M. intracellulare but could not distinguish between M. tuberculosis and M. bovis. PncA PCR assays were found specific in detecting the resp. ***mycobacterial*** species. The study confirms utility of pncA PCR assays in differential ***identification*** of M. tuberculosis and M. bovis and that of PRA of ***hsp65*** in the ***identification*** of M. avium.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Detection of ***Mycobacterium*** avium & M. tuberculosis from human sputum cultures by PCR-RFLP analysis of ***hsp65*** gene & pncA PCR

AB Background & objectives: ***Identification*** of ***mycobacteria*** by conventional methods is slow, labour intensive and may at times fail to produce precise results. Mol. techniques developed in the recent past, overcome these disadvantages facilitating rapid ***identification*** of most species. We undertook this study to characterize ***mycobacteria*** isolated from sputa of human patients suspected to have tuberculosis by conventional methods and later, by polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** gene and pncA PCR. Methods: Twenty two ***mycobacteria*** isolated from 30 sputum samples were ***identified*** based on growth rate, pigmentation, cultural and biochem. properties and subjected to PRA of ***hsp65*** gene involving amplification of ***hsp65*** gene and digestion of the product with BstEII and HaeIII in sep. reactions and anal. of digests by 3 per cent agarose gel electrophoresis. The ***mycobacteria*** were simultaneously evaluated by M.

tuberculosis-specific and M. bovis-specific pncA PCR assays in sep. reactions. Results: With the conventional biochem. tests, the 22 sputum culture isolates were ***identified*** as M. tuberculosis (19) and M. avium complex (MAC) (3). PCR of ***hsp65*** gene yielded 439 bp product in all the ***mycobacteria*** tested. The RFLP patterns of three MAC isolates with BstEII and HaeIII were identical to ref. M. avium strain with. . . digest. M. intracellulare ref. strain showed a distinct pattern with 3 fragments each in both enzyme digests. The PRA of ***hsp65*** confirmed MAC isolates as M. avium. M. tuberculosis isolates including H37Rv and M. bovis strains could not be discriminated by PRA of ***hsp65*** . The two pncA PCR assays (M. bovis-specific and M. tuberculosis-specific) detected specifically the resp. organisms with an amplification product of. . . bp. The MAC strains yielded no amplification product in both the pncA PCR assays. Interpretation & conclusion: PRA profiles of ***hsp65*** could differentiate MAC isolates into M. avium and M. intracellulare but could not distinguish between M. tuberculosis and M. bovis. PncA PCR assays were found specific in detecting the resp. ***mycobacterial*** species. The study confirms utility of pncA PCR assays in differential ***identification*** of M. tuberculosis and M. bovis and that of PRA of ***hsp65*** in the ***identification*** of M. avium.

ST PCR RFLP ***Mycobacterium*** tuberculosis ***diagnosis*** ***hsp65*** pncA

IT Sputum
(anal. sample; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Human
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Tuberculosis
(***diagnosis*** ; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Genotyping (method)
(discrimination between ***Mycobacterium*** species; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Alleles
(gene pncA, detection of; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT ***Diagnosis***
(mol.; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(pncA; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)
IT ***Diagnosis***
(tuberculosis; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)
IT 913767-99-4 913768-00-0 913768-01-1 913768-02-2 913768-03-3
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)
IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

L9 ANSWER 31 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:329492 CAPLUS <<LOGINID::20090617>>
DN 145:370383
TI Application of four molecular typing methods for analysis of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections
AU Sampaio, J. L. M.; Chimara, E.; Ferrazoli, L.; da Silva Telles, M. A.; Del Guercio, V. M. F.; Jerico, Z. V. N.; Miyashiro, K.; Fortaleza, C. M. C. B.; Padoveze, M. C.; Leao, S. C.
CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Sao Paulo, Sao Paulo, Brazil
SO Clinical Microbiology and Infection (2006), 12(2), 142-149
CODEN: CMINFM; ISSN: 1198-743X
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB A cluster of cases of post-augmentation mammaplasty surgical site infections occurred between 2002 and 2004 in Campinas, in the southern region of Brazil. Rapidly growing ***mycobacteria*** were isolated from samples from 12 patients. Eleven isolates were ***identified*** as ***Mycobacterium*** fortuitum and one as ***Mycobacterium*** porcinum by PCR-restriction digestion of the ***hsp65*** gene. These 12 isolates, plus six addnl. M. fortuitum isolates from non-related patients, were typed by pulsed-field gel electrophoresis (PFGE) and three PCR-based techniques: 16S-23S rRNA internal transcribed spacer (ITS) genotyping; randomly amplified polymorphic DNA (RAPD) PCR; and enterobacterial repetitive intergenic consensus (ERIC) PCR. Four novel M. fortuitum allelic variants were ***identified*** by restriction anal. of the ITS fragment. One major cluster, comprising six M. fortuitum isolates, and a second cluster of two isolates, were ***identified***

by the four methods. RAPD-PCR and ITS genotyping were less discriminative than ERIC-PCR. ERIC-PCR was comparable to PFGE as a valuable complementary tool for investigation of this type of outbreak.

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Application of four molecular typing methods for analysis of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections

AB . . . post-augmentation mammaplasty surgical site infections occurred between 2002 and 2004 in Campinas, in the southern region of Brazil. Rapidly growing ***mycobacteria*** were isolated from samples from 12 patients. Eleven isolates were ***identified*** as ***Mycobacterium*** fortuitum and one as ***Mycobacterium*** porcinum by PCR-restriction digestion of the ***hsp65*** gene. These 12 isolates, plus six addnl. M. fortuitum isolates from non-related patients, were typed by pulsed-field gel electrophoresis (PFGE). . . randomly amplified polymorphic DNA (RAPD) PCR; and enterobacterial repetitive intergenic consensus (ERIC) PCR. Four novel M. fortuitum allelic variants were ***identified*** by restriction anal. of the ITS fragment. One major cluster, comprising six M. fortuitum isolates, and a second cluster of two isolates, were ***identified*** by the four methods. RAPD-PCR and ITS genotyping were less discriminative than ERIC-PCR. ERIC-PCR was comparable to PFGE as a. . .

ST ***Mycobacterium*** post mammaplasty infection isolate analysis PCR PFGE; human post mammaplasty infection ***Mycobacterium*** species ***identification*** ***hsp65*** PCR; PCR PFGE comparison ***Mycobacterium*** analysis post mammaplasty infection

IT RAPD analysis
(-PCR; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Repetitive DNA
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ERIC (enterobacterial repetitive intergenic consensus); comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections)

IT Genetic element
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ITS (internal transcribed spacer); comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT PCR (polymerase chain reaction)
(ITS-, RAPD- and ERIC-; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium***

fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT ***Mycobacterium*** fortuitum
Mycobacterium porcinum
(***Mycobacterium*** species ***identification*** of isolates obtained from 12 patients with post-mammaplasty infections in Campinas, including ***Mycobacterium*** fortuitum and M. porcinum)

IT Mammary gland
(augmentation of, mammaplasty; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Human
(comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas)

IT Population genetics
(comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; ***Mycobacterium*** species ***identification*** of isolates obtained from patients with post-mammaplasty infections in Campinas using ***hsp65*** gene-specific PCR-restriction digestion anal.)

IT Evolution
(mol.; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Surgery
(plastic, augmentation mammaplasty; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Gel electrophoresis
(pulsed-field; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

L9 ANSWER 32 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:158391 CAPLUS <<LOGINID::20090617>>
DN 145:263808
TI ***Identification*** of ***Mycobacterium*** marinum 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma

AU Cai, Lin; Xue, Chen; Zhao, Ting; Ding, Bei-chuan; Zhang, Jian-zhong
CS Department of Dermatology, Peking University People's Hospital, Beijing, 100044, Peop. Rep. China
SO Chinese Medical Journal (Beijing, China, English Edition) (2006), 119(1), 43-48
CODEN: CMJODS; ISSN: 0366-6999
PB Chinese Medical Association
DT Journal
LA English
AB Nontuberculous ***mycobacterium*** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ***Mycobacterium*** marinum (M. marinum) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for detection and ***identification*** of M. marinum from lesions of patients with suspected M. marinum infections. Specimens were obtained from 5 patients with swimming pool granuloma. DNA was extd. and polymerase chain reaction (PCR) was performed. PCR products were digested with Hae III and BstE II, then analyzed by pattern restriction anal. to detect heat shock protein (hsp) 65 kD gene. The 65 kD hsp gene was found in all specimens from patients with swimming pool granuloma. PCR restriction anal. (PRA) ***identified*** all 5 samples to be M. marinum infections, and the result was consistent with that of routine bacteriol. ***identification*** . The lesions subsided or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in ***identification*** of ***mycobacteria*** . Application of this method will be helpful for early ***diagnosis*** of ***mycobacterial*** skin infections.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Identification*** of ***Mycobacterium*** marinum 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma
AB Nontuberculous ***mycobacterium*** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ***Mycobacterium*** marinum (M. marinum) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for detection and ***identification*** of M. marinum from lesions of patients with suspected M. marinum infections. Specimens were obtained from 5 patients with swimming. . . The 65 kD hsp gene was found in all specimens from patients with swimming pool granuloma. PCR restriction anal. (PRA) ***identified*** all 5 samples to be M. marinum infections, and the result was consistent with that of routine bacteriol. ***identification*** . The lesions subsided or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in ***identification*** of ***mycobacteria*** . Application of this method will be helpful for early ***diagnosis*** of ***mycobacterial*** skin infections.
ST gene ***hsp65*** specific PCR ***Mycobacterium*** detection human granuloma; PCR restriction enzyme analysis ***hsp65*** specific ***Mycobacterium*** detection
IT PCR (polymerase chain reaction)
(-restriction enzyme anal.; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, Tb11 and Tb12; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT Human
Mycobacterium marinum
(gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT Skin, disease
(lesion; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT ***Diagnosis***
(mol.; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , Tb11 and Tb12; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)
IT Granuloma
(swimming pool; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)

L9 ANSWER 33 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:620828 CAPLUS <<LOGINID::20090617>>
DN 144:206426
TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Bum-Joon
CS Department of Microbiology and Liver Research Institute, College of Medicine, Seoul National University Chongno-gu, 28 Yongon-dong, Chongno-gu, Seoul, 110-799, S. Korea
SO Journal of Microbiological Methods (2005), 62(2), 199-209
CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier B.V.
DT Journal
LA English
AB A method based on PCR-restriction fragment length polymorphism anal. (PRA)

using a novel region of the ***hsp65*** gene was developed for the rapid and exact ***identification*** of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of M. avium, M. intracellulare and M. tuberculosis to the species level by AvaII digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clin. isolates, which had been characterized by conventional biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the ***identification*** of ***mycobacteria*** culture isolates at the species level.

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.

AB A method based on PCR-restriction fragment length polymorphism anal. (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact ***identification*** of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, AvaII, HphI, and HpaII. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of. . . by conventional biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the ***identification*** of ***mycobacteria*** culture isolates at the species level.

ST PCR RFLP algorithm ***hsp65*** gene restriction endonuclease ***Mycobacterium***

IT Heat-shock proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(HSP 65; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

IT Algorithm
Human
Mycobacterium
Mycobacterium avium
Mycobacterium intracellulare
Mycobacterium tuberculosis
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

IT 81295-07-0, Restriction endonuclease AvaII 81295-25-2, Restriction endonuclease HpaII 81295-26-3, Restriction endonuclease HphI

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

IT 875804-98-1
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** HSPF3; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

IT 875804-99-2
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** HSPR4; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)

L9 ANSWER 34 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:224080 CAPLUS <<LOGINID::20090617>>
DN 143:279951
TI Comparative evaluation of polymerase chain reaction and restriction enzyme analysis: Two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***
AU Cheunoy, Wattana; Prammananan, Therdsak; Chaiprasert, Angkana; Foongladda, Suporn
CS Department of Microbiology, Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, 10700, Thailand
SO Diagnostic Microbiology and Infectious Disease (2005), 51(3), 165-171
CODEN: DMIDDZ; ISSN: 0732-8893
PB Elsevier Inc.
DT Journal
LA English
AB The increasing incidence of tuberculosis and other ***mycobacterial*** infections due to AIDS epidemic resulted in the need of rapid and accurate ***identification*** of isolated ***mycobacteria*** . The correct ***identification*** result leads to the selection of an appropriate therapeutic regimen. Polymerase chain reaction and restriction enzyme anal. (PCR-REA) has been developed since 1992 and used as the rapid method for ***identifying*** ***mycobacteria*** . Several genes or sequences have been used as an amplified target for PCR-REA. The present study aims to evaluate the potential use of PCR-REA of gene-encoding heat shock protein 65 kDa (***hsp65***) and .beta.-subunit RNA polymerase (rpoB) for the ***identification*** of ***mycobacteria*** compared with conventional biochem. ***identification*** . Two hundreds clin. isolates, consisting of 50 isolates of ***Mycobacterium*** tuberculosis and 150 isolates of nontuberculous ***mycobacteria*** (NTM), were submitted for ***identification*** using PCR-REA and biochem. method. The results demonstrated that PCR-REA ***identified*** 188 isolates of both M. tuberculosis and NTM concordantly with biochem. ***identification*** . Discordant ***identification*** results obtained from 12 isolates, comprised of 8 M. scrofulaceum, 1 M. avium complex, 1 M. malmoense, 1 M. terrae complex, and 1 M. chelonae/abscessus. Overall, the concordant percentage of results obtained from PCR-REA compared with biochem. method was 100%, 98.8%, and 83.3% for M. tuberculosis complex, rapidly growing, and slowly growing ***mycobacteria*** , resp., and the results of ***hsp65*** PCR-REA was in agreement with those obtained from rpoB PCR-REA. From this study,

PCR-REA appears to be a simple, rapid, and reliable method for ***identifying*** ***mycobacteria*** in a routine microbiol. lab.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Comparative evaluation of polymerase chain reaction and restriction enzyme analysis: Two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***

AB The increasing incidence of tuberculosis and other ***mycobacterial*** infections due to AIDS epidemic resulted in the need of rapid and accurate ***identification*** of isolated ***mycobacteria*** . The correct ***identification*** result leads to the selection of an appropriate therapeutic regimen. Polymerase chain reaction and restriction enzyme anal. (PCR-REA) has been developed since 1992 and used as the rapid method for ***identifying*** ***mycobacteria*** . Several genes or sequences have been used as an amplified target for PCR-REA. The present study aims to evaluate the potential use of PCR-REA of gene-encoding heat shock protein 65 kDa (***hsp65***) and .beta.-subunit RNA polymerase (rpoB) for the ***identification*** of ***mycobacteria*** compared with conventional biochem. ***identification*** . Two hundreds clin. isolates, consisting of 50 isolates of ***Mycobacterium*** tuberculosis and 150 isolates of nontuberculous ***mycobacteria*** (NTM), were submitted for ***identification*** using PCR-REA and biochem. method. The results demonstrated that PCR-REA ***identified*** 188 isolates of both M. tuberculosis and NTM concordantly with biochem. ***identification*** . Discordant ***identification*** results obtained from 12 isolates, comprised of 8 M. scrofulaceum, 1 M. avium complex, 1 M. malmoense, 1 M. terrae. . . from PCR-REA compared with biochem. method was 100%, 98.8%, and 83.3% for M. tuberculosis complex, rapidly growing, and slowly growing ***mycobacteria*** , resp., and the results of ***hsp65*** PCR-REA was in agreement with those obtained from rpoB PCR-REA. From this study, PCR-REA appears to be a simple, rapid, and reliable method for ***identifying*** ***mycobacteria*** in a routine microbiol. lab.

ST PCR RFLP ***identification*** ***Mycobacterium*** human infection

IT RFLP (restriction fragment length polymorphism)
(PCR; comparative evaluation of polymerase chain reaction and restriction enzyme anal. using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT ***Mycobacterium*** abscessus
Mycobacterium avium
Mycobacterium malmoense
Mycobacterium scrofulaceum
Mycobacterium terrae
Mycobacterium tuberculosis
(comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)

(***hsp65*** ; comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT Human
(infection; comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT ***Diagnosis***
(mol.; comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT PCR (polymerase chain reaction)
(restriction enzyme anal. (PCR-REA); comparative evaluation of polymerase chain reaction and restriction enzyme anal. using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(rpoB; comparative evaluation of polymerase chain reaction and restriction enzyme analysisusing two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

L9 ANSWER 35 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:171452 CAPLUS <<LOGINID::20090617>>
DN 143:279938
TI Multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme analysis in laboratories from Latin America and the Caribbean
AU Leao, Sylvia Cardoso; Bernardelli, Amelia; Cataldi, Angel; Zumarraga, Martin; Robledo, Jaime; Realpe, Teresa; Mejia, Gloria Isabel; Da Silva Telles, Maria Alice; Chimara, Erica; Velazco, Maritza; Fernandez, Jorge; Rodrigues, Pamela Araya; Guerrero, Martha Inirida; Leon, Clara Ines; Porras, Tania Bibiana; Rastogi, Nalin; Goh, Khye Seng; Suffys, Philip; Da Silva Rocha, Adalgisa; Dos Santos Netto, Diogo; Ritacco, Viviana; Lopez, Beatriz; Barrera, Lucia; Palomino, Juan Carlos; Martin, Anandi; Portaels, Francoise
CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Sao Paulo-Escola Paulista de Medicina, Sao Paulo, 04023-062, Brazil
SO Journal of Microbiological Methods (2005), 61(2), 193-199
CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier B.V.
DT Journal
LA English
AB The ***identification*** of ***mycobacterial*** species in clin. isolates is essential for making patient care decisions. Polymerase chain reaction (PCR) restriction enzyme anal. (PRA) is a simple and rapid ***identification*** method, based on amplification of 441 bp of the ***hsp65*** gene and restriction with BstEII and HaeIII. As a contribution to the validation of PRA, a multicenter study was performed in eight labs. located in Argentina, Brazil, Colombia, Chile, and Guadeloupe. Each lab. received 18 coded isolates from the collection of the Institute of Tropical Medicine (Antwerp, Belgium), representing

duplicates of nine lab. strains: ***Mycobacterium*** terrae CIPT 140320001, ***Mycobacterium*** scrofulaceum CIPT 140220031, ***Mycobacterium*** flavescens ATCC 14474, ***Mycobacterium*** triviale ATCC 23292, ***Mycobacterium*** nonchromogenicum ATCC 19530, ***Mycobacterium*** chitae ATCC 19627, ***Mycobacterium*** abscessus ATCC 19977, ***Mycobacterium*** kansasii ATCC 12478, and ***Mycobacterium*** peregrinum ATCC 14467. A detailed protocol including amplification, enzymic digestion, and gel prepn. was provided to each lab. Two labs. ***identified*** correctly all 18 (100%) isolates, one ***identified*** correctly 17 (94.5%), two ***identified*** 14 (77.7%), one ***identified*** 11 (61%), and two ***identified*** 8 (44.4%) isolates. Errors detected in labs. with more than 77% accuracy were assocd. with electrophoresis running conditions and an unspecific amplicon produced by a single strain. Lower accuracy was mainly related to inappropriate use of DNA markers and insufficient training in interpretation of patterns. In conclusion, the PRA method was readily implemented in some Latin American and Caribbean labs. of ***mycobacteria*** , but improvements in crit. points, as gel running conditions and training in interpretation of patterns, are needed in order to improve accuracy. In others, improvement in crit. points is still necessary.

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme analysis in laboratories from Latin America and the Caribbean

AB The ***identification*** of ***mycobacterial*** species in clin. isolates is essential for making patient care decisions. Polymerase chain reaction (PCR) restriction enzyme anal. (PRA) is a simple and rapid ***identification*** method, based on amplification of 441 bp of the ***hsp65*** gene and restriction with BstEII and HaeIII. As a contribution to the validation of PRA, a multicenter study was performed. . . 18 coded isolates from the collection of the Institute of Tropical Medicine (Antwerp, Belgium), representing duplicates of nine lab. strains: ***Mycobacterium*** terrae CIPT 140320001, ***Mycobacterium*** scrofulaceum CIPT 140220031, ***Mycobacterium*** flavescens ATCC 14474, ***Mycobacterium*** triviale ATCC 23292, ***Mycobacterium*** nonchromogenicum ATCC 19530, ***Mycobacterium*** chitae ATCC 19627, ***Mycobacterium*** abscessus ATCC 19977, ***Mycobacterium*** kansasii ATCC 12478, and ***Mycobacterium*** peregrinum ATCC 14467. A detailed protocol including amplification, enzymic digestion, and gel prepn. was provided to each lab. Two labs. ***identified*** correctly all 18 (100%) isolates, one ***identified*** correctly 17 (94.5%), two ***identified*** 14 (77.7%), one ***identified*** 11 (61%), and two ***identified*** 8 (44.4%) isolates. Errors detected in labs. with more than 77% accuracy were assocd. with electrophoresis running conditions and an. . . in interpretation of patterns. In conclusion, the PRA method was readily implemented in some Latin American and Caribbean labs. of ***mycobacteria*** , but improvements in crit. points, as gel running conditions and training in interpretation of patterns, are needed in order to. . .

ST ***Mycobacterium*** PCR restriction enzyme analysis

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)

(***hsp65*** ; multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme anal. in labs. from Latin America and Caribbean)

IT ***Mycobacterium***
Mycobacterium abscessus
Mycobacterium chitae
Mycobacterium flavescens
Mycobacterium kansasii
Mycobacterium nonchromogenicum
Mycobacterium peregrinum
Mycobacterium scrofulaceum
Mycobacterium terrae
Mycobacterium triviale
PCR (polymerase chain reaction)
(multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme anal. in labs. from Latin America and Caribbean)

IT 81295-18-3 93229-61-9, Restriction endonuclease, BstEII
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme anal. in labs. from Latin America and Caribbean)

IT 864193-17-9 864193-18-0
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme anal. in labs. from Latin America and Caribbean)

L9 ANSWER 36 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:81792 CAPLUS <<LOGINID::20090617>>
DN 143:20521
TI Rapid species ***identification*** within the ***Mycobacterium*** chelonae-abscessus group by high-resolution melting analysis of ***hsp65*** PCR products
AU Odell, Ian D.; Cloud, Joann L.; Seipp, Michael; Wittwer, Carl T.
CS Department of Pathology, University of Utah Medical School, Salt Lake City, USA
SO American Journal of Clinical Pathology (2005), 123(1), 96-101
CODEN: AJCPAI; ISSN: 0002-9173
PB American Society of Clinical Pathology
DT Journal
LA English
AB Polymerase chain reaction (PCR) amplification of the heat shock protein 65 (***hsp65***) gene followed by high-resoln. melting anal. with LCGreen I (Idaho Technol., Salt Lake City, UT) was used to differentiate the ***mycobacteria*** species ***Mycobacterium*** chelonae, ***Mycobacterium*** abscessus, and ***Mycobacterium*** immunogenum in less than 20 min. A 105-base-pair amplicon that clustered the different species by predicted melting temp. was found from available GenBank ***hsp65*** sequences. We ***identified*** 24 clin. isolates within the M chelonae-abscessus group by proximal 16S rRNA and ***hsp65*** gene sequencing. Rapid-cycle PCR followed by high-resoln. melting anal. clustered these samples into the following groups: M abscessus, 12; M abscessus sequence variant, 2; M chelonae, 7; unexpected

M chelonae sequence variant, 1; and M immunogenum, 2. The M chelonae variant had a single base change not found in reported GenBank sequences. Advantages of the method include speed, low risk of amplicon contamination (closed-tube), and no need for sepn. steps (sequencing, electrophoresis, high-performance liq. chromatog.) or real-time monitoring.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Rapid species ***identification*** within the ***Mycobacterium*** chelonae-abscessus group by high-resolution melting analysis of ***hsp65*** PCR products

AB Polymerase chain reaction (PCR) amplification of the heat shock protein 65 (***hsp65***) gene followed by high-resoln. melting anal. with LCGreen I (Idaho Technol., Salt Lake City, UT) was used to differentiate the ***mycobacteria*** species ***Mycobacterium*** chelonae, ***Mycobacterium*** abscessus, and ***Mycobacterium*** immunogenum in less than 20 min. A 105-base-pair amplicon that clustered the different species by predicted melting temp. was found from available GenBank ***hsp65*** sequences. We ***identified*** 24 clin. isolates within the M chelonae-abscessus group by proximal 16S rRNA and ***hsp65*** gene sequencing. Rapid-cycle PCR followed by high-resoln. melting anal. clustered these samples into the following groups: M abscessus, 12; M. . .

ST PCR melting analysis ***Mycobacterium*** gene ***hsp65***

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Nucleic acid hybridization
(melting anal.; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT ***Diagnosis***
(mol.; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Human
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium immunogenum

PCR (polymerase chain reaction)
(species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Genotyping (method)

(species ***identification*** ; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT 853031-88-6 853031-89-7
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

L9 ANSWER 37 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:69709 CAPLUS <<LOGINID::20090617>>
DN 143:1806
TI A new method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on amplified ***hsp65*** restriction analysis (AHSPRA)
AU Selvaraju, Suresh B.; Khan, Izhar U. H.; Yadav, Jagjit S.
CS Molecular Toxicology Division, Department of Environmental Health, University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA
SO Molecular and Cellular Probes (2005), 19(2), 93-99
CODEN: MCPRE6; ISSN: 0890-8508
PB Elsevier B.V.
DT Journal
LA English
AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M. chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium*** immunogenum, have been implicated in nosocomial infections and occupational respiratory illnesses like hypersensitivity pneumonitis (HP) assocd. with contaminated metalworking fluid (MWF) exposures. Close relationship among these member species makes their differentiation cumbersome using the existing methods. Here we report a simple and rapid method for unambiguous ***identification*** and differentiation of the three-member species of the MCC group with PCR-restriction anal. targeting a 667-bp segment of a variable region of the 65-kDa-heat shock protein (***hsp65***) gene. This assay, described as Amplified ***hsp65*** Restriction Anal. (AHSPRA), can discriminate all the three individual species using a one-step restriction digestion using either BbvI or Eco0109I. The enzyme NarI can differentiate M. immunogenum from the other two MCC species (M. chelonae and M. abscessus). The developed method was validated using several non-MCC ref. species of other rapidly growing ***mycobacteria*** (RGM) and MCC field isolates from MWF samples. Direct cell-lysis was used instead of the conventional DNA template prepn., which improved the rapidity, simplicity and adaptability of the developed method. The results suggest that the developed method can unambiguously differentiate species of the M. chelonae complex from other RGM species and from one another.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI A new method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on amplified ***hsp65*** restriction analysis (AHSPRA)
AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M. chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium*** immunogenum, have been implicated in nosocomial infections and occupational respiratory illnesses like hypersensitivity pneumonitis (HP) assocd. with contaminated metalworking fluid. . . member species makes their differentiation cumbersome using the existing methods. Here we

report a simple and rapid method for unambiguous ***identification*** and differentiation of the three-member species of the MCC group with PCR-restriction anal. targeting a 667-bp segment of a variable region of the 65-kDa-heat shock protein (***hsp65***) gene. This assay, described as Amplified ***hsp65*** Restriction Anal. (AHSPRA), can discriminate all the three individual species using a one-step restriction digestion using either BbvI or Eco0109I.. . . species (M. chelonae and M. abscessus). The developed method was validated using several non-MCC ref. species of other rapidly growing ***mycobacteria*** (RGM) and MCC field isolates from MWF samples. Direct cell-lysis was used instead of the conventional DNA template prepn., which. . .

ST sequence ***Mycobacterium*** gene ***hsp65*** PCR ***diagnosis***

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HSP 65; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT DNA sequences
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium immunogenum
PCR (polymerase chain reaction)
Protein sequences
RFLP (restriction fragment length polymorphism)
Respiratory system, disease
(PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT Human
(***diagnosis*** in; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT ***Diagnosis***
(mol.; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT 852345-32-5 852345-33-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT 824883-12-7 824883-14-9 824883-16-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(amino acid sequence; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)
IT 824883-11-6 824883-13-8 824883-15-0
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

L9 ANSWER 38 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:973914 CAPLUS <<LOGINID::20090617>>
DN 142:170995
TI Method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction
IN Kim, Eun Ha; Park, Yeong Seok
PA Biocore Co., Ltd., S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given
CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI KR 2003075315	A	20030926	KR 2002-14466	20020318
PRAI KR 2002-14466		20020318		

AB A method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) by multiple-nested polymerase chain reaction is provided, thereby rapidly detecting tubercle Bacillus and nontuberculous ***Mycobacteria*** . A method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) comprises carrying out multiple-nested polymerase chain reaction using all of three kinds of ***primer*** pairs specific to mtp40, IS6110 and ***hsp65*** , resp., which are assocd. with ***Mycobacteria*** , wherein the ***primer*** pairs have the nucleotide sequences of SEQ ID NOs: 1 to 12. The method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) comprises the steps of: adding DNA extd. from infected microorganism and three kinds of ***primers*** of SEQ ID NOs: 1 to 12 into a patient's sample; amplifying a portion or the total of the gene by multiple-nested polymerase chain reaction; and analyzing the amplified products.
TI Method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction
AB A method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) by multiple-nested polymerase chain reaction is provided, thereby rapidly detecting tubercle Bacillus and nontuberculous ***Mycobacteria*** . A method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) comprises carrying out multiple-nested polymerase chain reaction using all of three kinds of ***primer*** pairs specific to mtp40, IS6110 and ***hsp65*** , resp., which are assocd. with ***Mycobacteria*** , wherein the ***primer*** pairs

have the nucleotide sequences of SEQ ID NOs: 1 to 12. The method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) comprises the steps of: adding DNA extd. from infected microorganism and three kinds of ***primers*** of SEQ ID NOs: 1 to 12 into a patient's sample; amplifying a portion or the total of the gene. . .

ST Tubercle bacillus nontuberculous ***mycobacteria*** ***diagnosis*** ***primer*** PCR

IT Gene, microbial
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(IS6110; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT Gene, microbial
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(***hsp65*** ; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Diagnosis***
Mycobacterium tuberculosis
(method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT Gene, microbial
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(mtp40; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT PCR (polymerase chain reaction)
(nested; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Mycobacterium***
(nontuberculous; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT DNA sequences
(of ***primers*** ; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

L9 ANSWER 39 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:727349 CAPLUS <<LOGINID::20090617>>
DN 142:87110
TI Capillary electrophoretic restriction fragment length polymorphism patterns for the ***mycobacterial*** ***hsp65*** gene
AU Ho, Hsin-Tsung; Chang, Po-Ling; Hung, Chia-Chien; Chang, Huan-Tsung
CS Department of Laboratory Medicine, Mackay Memorial Hospital, Taipei,

Taiwan
SO Journal of Clinical Microbiology (2004), 42(8), 3525-3531
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe method for the rapid ***identification*** of ***Mycobacterium*** species. We demonstrate the sepn. of DNA or restriction fragments digested from the ***mycobacterial*** gene encoding the 65-kDa heat shock protein (***hsp65***) by capillary electrophoresis (CE). By using a pair of unlabeled ***primers*** , Tb11 and Tb12, and only one restriction enzyme, HaeIII, we investigated a total of 52 ref. and clin. strains encompassing 12 ***Mycobacterium*** species. The electrophoretic sepn. of high-resoln. CE required <20 min and was capable of ***identifying*** fragments as small as 12 bp. A good agreement of measurement was obsd. between the sizes of restriction fragments resolved by CE, and the real sizes were deduced from the sequence anal. Distinct differentiations were also well demonstrated between some species and subspecies by an extra HaeIII digestion site. With the advantage of the complete RFLP pattern available from CE, it appears to be more convenient to use an electropherogram rather than performing the cumbersome slab gel electrophoresis plus ***diagnostic*** algorithm to ***identify*** ***Mycobacterium*** species. Beyond the agarose and polyacrylamide gel electrophoresis, high-resoln. CE provides an alternative for rapid ***identification*** of ***Mycobacterium*** species that is feasible
for automation and routine use without the need for costly probes.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Capillary electrophoretic restriction fragment length polymorphism patterns for the ***mycobacterial*** ***hsp65*** gene
AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe method for the rapid ***identification*** of ***Mycobacterium*** species. We demonstrate the sepn. of DNA or restriction fragments digested from the ***mycobacterial*** gene encoding the 65-kDa heat shock protein (***hsp65***) by capillary electrophoresis (CE). By using a pair of unlabeled ***primers*** , Tb11 and Tb12, and only one restriction enzyme, HaeIII, we investigated a total of 52 ref. and clin. strains encompassing 12 ***Mycobacterium*** species. The electrophoretic sepn. of high-resoln. CE required <20 min and was capable of ***identifying*** fragments as small as 12 bp. A good agreement of measurement was obsd. between the sizes of restriction fragments resolved. . . CE, it appears to be more convenient to use an electropherogram rather than performing the cumbersome slab gel electrophoresis plus ***diagnostic*** algorithm to ***identify*** ***Mycobacterium*** species. Beyond the agarose and polyacrylamide gel electrophoresis, high-resoln. CE provides an alternative for rapid ***identification*** of ***Mycobacterium*** species that is feasible for automation and routine use without the need for costly probes.
ST RFLP capillary electrophoresis genotyping ***Mycobacterial*** ***hsp65*** gene
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65, gene for; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)

IT PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(PCR-RFLP; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)
IT Capillary electrophoresis
Genotyping (method)
Mycobacterium
Mycobacterium abscessus
Mycobacterium asiaticum
Mycobacterium avium
Mycobacterium chelonae chelonae
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium gordonae
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium phlei
Mycobacterium smegmatis
Mycobacterium tuberculosis
(capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)
IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(for heat shock protein ***hsp65*** ; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)
IT Human
(human infection; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)
IT 81295-18-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)

L9 ANSWER 40 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:715776 CAPLUS <<LOGINID::20090617>>
DN 142:255259
TI LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae
AU Sedlacek, L.; Rifai, M.; Feldmann, K.; Bange, F. C.
CS Department of Medical Microbiology and Hospital Epidemiology, Medical School Hannover, Hannover, 30625, Germany
SO Journal of Clinical Microbiology (2004), 42(7), 3284-3287
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB In this study we introduce a rapid procedure to ***identify*** ***Mycobacterium*** abscessus (types I and II) and M. chelonae using LightCycler-based anal. of the ***hsp65*** gene. Results from 36 clin. strains were compared with ***hsp65*** gene restriction anal. and biochem. profiles of bacilli. As all three methods yielded identical results for each isolate, this procedure offers an excellent alternative to previously established nucleic acid amplification-based techniques for the ***diagnosis*** of ***mycobacterial*** diseases.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae

AB In this study we introduce a rapid procedure to ***identify*** ***Mycobacterium*** abscessus (types I and II) and M. chelonae using LightCycler-based anal. of the ***hsp65*** gene. Results from 36 clin. strains were compared with ***hsp65*** gene restriction anal. and biochem. profiles of bacilli. As all three methods yielded identical results for each isolate, this procedure offers an excellent alternative to previously established nucleic acid amplification-based techniques for the ***diagnosis*** of ***mycobacterial*** diseases.

ST ***Mycobacterium*** differentiation LightCycler PCR ***primer*** probe sequence; ***hsp65*** 16S rRNA gene detection PCR ***Mycobacterium***

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S rRNA; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S, gene; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT ***Mycobacterium*** abscessus
Mycobacterium chelonae
(LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT DNA sequences
(PCR ***primers*** ; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT RFLP (restriction fragment length polymorphism)
(RFLP-PCR; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT ***Diagnosis***
(mol.; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT PCR (polymerase chain reaction)
(multiplex, LightCycler; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 245670-26-2D, LC Red 640, conjugates with hybridization probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(LC Red 640; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 251949-03-8D, LC-RED 705, conjugates with hybridization probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL

(Biological study); USES (Uses)
(LC Red 705; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 2321-07-5D, Fluorescein, conjugates with hybridization probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-14-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** sequence, Tb_11; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-15-0
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** sequence, Tb_12; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-18-3D, 3'-conjugate with fluorescein
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe sequence, LC_68; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-19-4D, 5'-conjugate with LightCycler Red 705
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe sequence, LC_86; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-16-1D, 3'-conjugate with fluorescein
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe sequence, LC_98; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 845683-17-2D, 5'-conjugate with LightCycler Red 640
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe sequence, LC_99; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 7647-14-5, Sodium chloride, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(tolerance, of ***Mycobacterium*** ; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

IT 994-36-5, Sodium citrate
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(utilization, by ***Mycobacterium*** ; LightCycler-based differentiation of ***Mycobacterium*** abscessus and ***Mycobacterium*** chelonae)

L9 ANSWER 41 OF 71 CAPLUS

AN 2004:642461 CAPLUS <<LOGINID::20090617>>
DN 141:406390
TI Standardization of in-house polymerase chain reaction for the ***identification*** of ***Mycobacterium*** tuberculosis at the Reference Tropical Disease Hospital in the State of Goias, Brazil
AU Rodrigues, Marcia Alves Vasconcelos; Serafini, Alvaro Bisol; Pereira, Marieta de Souza; Dias da Silva, Thathiane; Rabahi, Marcelo Fouad; Lemes de Alves, Suely; Kipnis, Andre
CS Departamento de Microbiologia, Instituto de Patologia Tropical e Saude Publica, Universidade Federal de Goias, Goiania, 74605-050, Brazil
SO Memorias do Instituto Oswaldo Cruz (2004), 99(4), 415-419
CODEN: MIOCAS; ISSN: 0074-0276
PB Instituto Oswaldo Cruz
DT Journal
LA English
AB This study compares smear, growth in Lowenstein-Jensen medium, and inhouse polymerase chain reaction (PCR) techniques for the detection of ***Mycobacterium*** tuberculosis. A total of 72 specimens from 72 patients with clin. symptoms of tuberculosis, including 70 sputum and two bronchial aspirate samples, were tested in parallel by smear, culture, and inhouse PCR techniques. From these, 48 (66.6%) were neg. by the 3 methods, 2 (2.8%) were smear pos. and neg. by culture and inhouse PCR, 11 (15.3%) were both smear and culture neg., and inhouse PCR pos., 7 (9.7%) were pos. by the 3 methods, 2 (2.8%) were pos. by smear and culture, and neg. by PCR, 2 (2.8%) were pos. by culture and PCR, but smear neg. After the resoln. of discrepancies in PCR results, the sensitivity and specificity for inhouse PCR technique to M. tuberculosis relative to the culture, were 81.8% and 81.9%, resp. These results confirm that this method, inhouse PCR, may be a sensitive and specific technique for M. tuberculosis detection, occurring in both pos. and neg. smear and neg. cultures.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Standardization of in-house polymerase chain reaction for the ***identification*** of ***Mycobacterium*** tuberculosis at the Reference Tropical Disease Hospital in the State of Goias, Brazil
AB This study compares smear, growth in Lowenstein-Jensen medium, and inhouse polymerase chain reaction (PCR) techniques for the detection of ***Mycobacterium*** tuberculosis. A total of 72 specimens from 72 patients with clin. symptoms of tuberculosis, including 70 sputum and two bronchial. . .
ST PCR ***Mycobacterium*** tuberculosis ***diagnosis*** gene ***hsp65***
IT ***Mycobacterium*** tuberculosis
Tuberculosis
(PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)
IT Sputum
(anal. matrix; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)
IT Bronchi
(aspirates, anal. matrix; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)
IT Human

(***diagnosis*** in; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(***hsp65*** ; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

IT ***Diagnosis***
(mol.; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

IT PCR (polymerase chain reaction)
(nested; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

IT 792989-28-7 792989-29-8 792989-30-1 792989-31-2
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** for ***Mycobacterium*** gene ***hsp65*** ; PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

L9 ANSWER 42 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:287934 CAPLUS <<LOGINID::20090617>>
DN 140:282411
TI Molecular size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme analysis
IN Koeksalan, Orhan Kaya; Kocagoez, Tanil
PA Turk.
SO PCT Int. Appl., 12 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004029296	A2	20040408	WO 2003-TR82	20030926
	WO 2004029296	A3	20040902		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2003276821	A1	20040419	AU 2003-276821	20030926
	TR 200501010	T2	20050523	TR 2005-1010	20030926
	US 20060121479	A1	20060608	US 2005-528453	20051011
PRAI	TR 2002-2252	A	20020926		
	WO 2003-TR82	W	20030926		

AB This invention consists of DNA mol. size markers which are used to det. in a correct and easy way the size of DNA fragments in the evaluation step of the sizes of DNA restriction fragments sepd. by electrophoresis, of the ***hsp65*** PCR-REA method used for species ***identification*** of ***mycobacteriae*** .

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Molecular size markers and methods for ***identification*** of

Mycobacteria species by PCR and restriction enzyme analysis

AB . . . size of DNA fragments in the evaluation step of the sizes of DNA restriction fragments sepd. by electrophoresis, of the ***hsp65*** PCR-REA method used for species ***identification*** of ***mycobacteriae*** .

ST ***Mycobacterium*** species ***identification*** PCR restriction enzyme analysis marker

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** , amplification of; mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

IT Gel electrophoresis
Molecular cloning
Mycobacterium
Mycobacterium chitae
Mycobacterium gallinarum
Mycobacterium intracellulare
Mycobacterium simiae
Mycobacterium smegmatis
Mycobacterium terrae
Mycobacterium tuberculosis
Mycobacterium xenopi
Nucleic acid amplification (method)
PCR (polymerase chain reaction)
Species differences
(mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

IT ***Diagnosis***
(mol.; mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

IT 675887-28-2 675887-29-3
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TB11 ***primer*** sequence; mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

IT 9075-08-5, Restriction enzyme 81295-18-3 93229-61-9, Restriction endonuclease, BstEII
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(mol. size markers and methods for ***identification*** of ***Mycobacteria*** species by PCR and restriction enzyme anal.)

L9 ANSWER 43 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:121485 CAPLUS <<LOGINID::20090617>>
DN 140:298231
TI Development of a single-tube, cell lysis-based, genus-specific PCR method for rapid ***identification*** of ***mycobacteria*** : optimization of cell lysis, PCR ***primers*** and conditions, and restriction pattern analysis

AU Khan, Izhar U. H.; Yadav, Jagjit S.
CS Molecular Toxicology Division, Department of Environmental Health, University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA
SO Journal of Clinical Microbiology (2004), 42(1), 453-457
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB A single-tube PCR method was developed for efficient ***identification*** of nontuberculous ***mycobacteria*** (NTM) and their environmental isolates in about 3 h without conventional DNA isolation. The following three steps were optimized or developed: (i) a simple, 6-min direct cell lysis protocol as a PCR prestep for generation of DNA-template; (ii) an improved ***Mycobacterium*** -specific PCR amplification protocol with a broader species specificity using newly designed ***primers*** targeting a 228-bp region of the 65-kDa heat shock protein (hsp) gene and optimal PCR amplification conditions; and (iii) a genus-specific restriction anal. of the PCR product for conclusive ***identification*** of the unknown NTM isolates.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Development of a single-tube, cell lysis-based, genus-specific PCR method for rapid ***identification*** of ***mycobacteria*** : optimization of cell lysis, PCR ***primers*** and conditions, and restriction pattern analysis
AB A single-tube PCR method was developed for efficient ***identification*** of nontuberculous ***mycobacteria*** (NTM) and their environmental isolates in about 3 h without conventional DNA isolation. The following three steps were optimized or. . . developed: (i) a simple, 6-min direct cell lysis protocol as a PCR prestep for generation of DNA-template; (ii) an improved ***Mycobacterium*** -specific PCR amplification protocol with a broader species specificity using newly designed ***primers*** targeting a 228-bp region of the 65-kDa heat shock protein (hsp) gene and optimal PCR amplification conditions; and (iii) a genus-specific restriction anal. of the PCR product for conclusive ***identification*** of the unknown NTM isolates.
ST DNA sequence gene hsp ***Mycobacterium*** isolate MJY3; protein ***HSP65*** sequence ***Mycobacterium*** isolate MJY3; gene hsp specific PCR restriction analysis ***identification*** nontuberculous ***mycobacteria***
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HSP 65; partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)
IT PCR (polymerase chain reaction)
(development and optimization of single-tube cell lysis-based gene hsp genus-specific PCR method for rapid ***identification*** of nontuberculous ***mycobacteria***)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hsp; development and optimization of single-tube cell lysis-based gene hsp genus-specific PCR method for rapid ***identification*** of nontuberculous ***mycobacteria***)
IT DNA sequences
(partial DNA sequence of 65-kDa heat shock protein gene hsp amplified from ***Mycobacterium*** strain M-JY3 using developed genus-specific PCR)
IT Protein sequences
(partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)
IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)
IT ***Mycobacterium***
(use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)
IT 638110-92-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)
IT 676577-44-9 676577-45-0 676577-46-1 676577-47-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene hsp-specific ***primer*** ; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)
IT 638110-91-5
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; partial DNA sequence of 65-kDa heat shock protein gene hsp amplified from ***Mycobacterium*** strain M-JY3 using developed genus-specific PCR)

L9 ANSWER 44 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:591378 CAPLUS <<LOGINID::20090617>>
DN 139:146183
TI ***Primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species
IN Kim, Bum-joon; Kook, Yoon-ho; Kim, Jeong-mi
PA Biomedlab Corporation, S. Korea
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an HSP 65 gene fragment, and a method for the ***identification*** of ***mycobacterial*** species by using the same. More specifically, the 604-bp HSP 65 gene fragment can be applied to ***identification*** methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional ***identification*** method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the ***identification*** method of the present invention, the ***mycobacterial*** species can be ***identified*** simply, economically, and accurately.

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an HSP 65 gene fragment, and a method for the ***identification*** of ***mycobacterial*** species by using the same. More specifically, the 604-bp HSP 65 gene fragment can be applied to ***identification*** methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional ***identification*** method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the ***identification*** method of the present invention, the ***mycobacterial*** species can be ***identified*** simply, economically, and accurately.

ST ***primer*** ***mycobacteria*** heat shock protein ***hsp65*** gene

IT Nucleic acid amplification (method)
(DNA; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(HSP 65; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HSP 65; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT ***Diagnosis***
(mol.; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium
Mycobacterium avium paratuberculosis
Mycobacterium bovis
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium leprae
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium microti
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium parafortuitum
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium simiae
Mycobacterium smegmatis

Mycobacterium szulgai
Mycobacterium terrae
Mycobacterium thermoresistibile
Mycobacterium triviale
Mycobacterium tuberculosis
Mycobacterium ulcerans
Mycobacterium vaccae
Mycobacterium wolinskyi
Nocardia carnea
RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
(***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
569432-52-6 569432-53-7 569432-54-8 569432-55-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT 569432-56-0
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** HSPF3 sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT 569432-57-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** HSPR3 sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

IT 569477-29-8
RL: PRP (Properties)
(unclaimed sequence; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

L9 ANSWER 45 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:88707 CAPLUS <<LOGINID::20090617>>
DN 137:227047
TI Application of molecular biology techniques to the ***diagnosis*** of nontuberculous ***mycobacterial*** infections
AU Ruiz, M.; Rodriguez, J. C.; Escribano, I.; Garcia-Martinez, J.; Rodriguez-Valera, F.; Royo, G.
CS S. Microbiologia, Hospital General Universitario de Elche, Alicante, 03203, Spain
SO APMIS (2001), 109(12), 857-864
CODEN: APMSEL; ISSN: 0903-4641
PB Munksgaard International Publishers Ltd.
DT Journal
LA English
AB A total of 19,723 clin. samples were cultivated for the detection of ***mycobacteria*** from Jan. 1995 to Mar. 2001. The 203 strains of nontuberculous ***mycobacteria*** isolated were ***identified*** with the use of mol. techniques in combination with traditional biochem. tests. The mol. methods applied were PCR-restriction fragment length polymorphism anal. (PRA) alone, or in combination with 16S rRNA and 16S-23S spacer sequencing. The patient records of those with specimens pos. for ***mycobacteria*** were analyzed to evaluate the clin. significance of the culture results. Twenty-five of the 124 patients analyzed (20%) were regarded as having clin. ***mycobacteriosis*** . The main species assocd. with ***mycobacteriosis*** were: ***Mycobacterium*** avium (13 cases), M. intracellulare (2 cases), M. kansasii (5 cases), M. chelonae (2 cases), M. malmoense (1 case), M. scrofulaceum (1 case) and M. marinum (1 case). The use of PRA alone or in combination with gene sequencing provided valuable help in discerning ***mycobacteria*** at both the intra- and interspecies level, thus contributing to a faster and more efficient ***diagnosis*** and epidemiol. follow-up.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Application of molecular biology techniques to the ***diagnosis*** of nontuberculous ***mycobacterial*** infections
AB A total of 19,723 clin. samples were cultivated for the detection of ***mycobacteria*** from Jan. 1995 to Mar. 2001. The 203 strains of nontuberculous ***mycobacteria*** isolated were ***identified*** with the use of mol. techniques in combination with traditional biochem. tests. The mol. methods applied were PCR-restriction fragment length. . . alone, or in combination with 16S rRNA and 16S-23S spacer sequencing. The patient records of those with specimens pos. for ***mycobacteria*** were analyzed to evaluate the clin. significance of the culture results. Twenty-five of the 124 patients analyzed (20%) were regarded as having clin. ***mycobacteriosis*** . The main species assocd. with ***mycobacteriosis*** were: ***Mycobacterium*** avium (13 cases), M.

intracellulare (2 cases), M. kansasii (5 cases), M. chelonae (2 cases), M. malmoense (1 case), M.. . . M. marinum (1 case). The use of PRA alone or in combination with gene sequencing provided valuable help in discerning ***mycobacteria*** at both the intra- and interspecies level, thus contributing to a faster and more efficient ***diagnosis*** and epidemiol. follow-up.

ST PCR RFLP 16S rDNA ITS sequence nontuberculous ***Mycobacterium*** detection; DNA sequence ***Mycobacterium*** 16S 23S rDNA ITS; ***primer*** ***diagnosis*** nontuberculous ***mycobacterial*** infection PCR RFLP; human Spain HIV ***Mycobacterium*** infection detection method PRA

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S; DNA sequence of complete 16S rRNA gene, ITS region, and partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(23 S; DNA sequence of complete 16S rRNA gene, ITS region, and partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT DNA sequences
Mycobacterium avium
(DNA sequence of complete 16S rRNA gene, ITS region, and partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ITS (internal transcribed spacer); use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples)

IT Human groups
(Spanish; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained in Spain)

IT Infection
(bacterial, ***mycobacteriosis*** ; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for ***diagnosis*** of nontuberculous ***mycobacterial*** infections)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for 16S rRNA; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for 23S RNA; DNA sequence of complete 16S rRNA gene, ITS region, and

partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

IT ***Diagnosis***
(mol.; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for ***diagnosis*** of nontuberculous ***mycobacterial*** infections)

IT Epidemiology
(mol.; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for ***diagnosis*** of nontuberculous ***mycobacterial*** infections, potential use in epidemiol.)

IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

IT Bone marrow
Feces
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples (such as bone marrow, and feces) obtained from patients also infected with HIV)

IT Blood analysis
Respiratory system
Urine analysis
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples (such as respiratory tract, urine, blood) obtained from patients also infected with HIV)

IT Pleural fluid
Skin
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples (such pleural fluid and skin) obtained from patients also infected with HIV)

IT Human immunodeficiency virus
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

IT Human
Mycobacterium chelonae
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium scrofulaceum

(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained in Spain)

IT 457965-27-4 457965-28-5 458571-15-8
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; use of PCR-RFLP (PRA) alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

IT 431974-46-8, GenBank AF410479
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; DNA sequence of complete 16S rRNA gene, ITS region, and partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

L9 ANSWER 46 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:647495 CAPLUS <<LOGINID::20090617>>
DN 136:304792
TI ***Identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene
AU Brunello, Francesca; Ligozzi, Marco; Cristelli, Emanuela; Bonora, Stefano; Tortoli, Enrico; Fontana, Roberta
CS Dipartimento di Patologia, Sezione di Microbiologia, Universita di Verona and Servizio di Microbiologia dell'Azienda Ospedaliera di Verona, Verona, 37100, Italy
SO Journal of Clinical Microbiology (2001), 39(8), 2799-2806
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding the 65-kDa heat shock protein. Restriction digests were sepd. by 10% polyacrylamide gel electrophoresis (PAGE). By including a size std. in each sample, the restriction fragment profile was calcd. using a computer-aided comparison program. An algorithm describing these 54 species (including 22 species not previously described) is proposed. We found that this assay based on 10% PAGE provided a more precise est. than that based on agarose gel electrophoresis of the real size of restriction fragments as deduced from the sequence anal. and allowed ***identification*** of ***mycobacteria*** whose PCR-restriction fragment length polymorphism anal. patterns were unequivocally ***identified*** by fragments shorter than 60 bp.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene
AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding. . . based on agarose gel electrophoresis of the real size of

restriction fragments as deduced from the sequence anal. and allowed ***identification*** of ***mycobacteria*** whose PCR-restriction fragment length polymorphism anal. patterns were unequivocally ***identified*** by fragments shorter than 60 bp.

ST DNA sequence ***Mycobacterium*** gene ***hsp65*** protein; genotyping PCR RFLP polyacrylamide gel electrophoresis algorithm ***Mycobacterium*** ***hsp65***

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HSP 65; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT RFLP (restriction fragment length polymorphism)
(PCR-; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene ***hsp65*** ; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT Algorithm
Gel electrophoresis
Genotyping (method)
Mycobacterium abscessus
Mycobacterium agri
Mycobacterium aichiense
Mycobacterium alvei
Mycobacterium asiaticum
Mycobacterium austroafricanum
Mycobacterium avium
Mycobacterium avium paratuberculosis
Mycobacterium branderi
Mycobacterium brumae
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium confluentis
Mycobacterium duvalii
Mycobacterium fallax
Mycobacterium farcinogenes
Mycobacterium fortuitum
Mycobacterium gadium
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gilvum
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium hiberniae

Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium obuense
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium porcinum
Mycobacterium poriferae
Mycobacterium pulveris
Mycobacterium rhodesiae
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium siernhoferi
Mycobacterium simiae
Mycobacterium smegmatis
Mycobacterium szulgai

PCR (polymerase chain reaction)
(***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT Protein sequences
(of gene ***hsp65*** heat shock protein isolated from ***Mycobacterium*** species)

IT DNA sequences
(of gene ***hsp65*** isolated from ***Mycobacterium*** species)

IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT 409133-45-5 409133-46-6 409133-47-7 409133-48-8 409133-49-9
409133-50-2 409133-51-3 409133-52-4 409133-53-5 409133-54-6
409133-55-7 409133-56-8 409133-57-9 409133-58-0 409133-59-1
409133-60-4 409133-61-5 409133-62-6 409133-63-7 409133-64-8
409133-65-9 409133-66-0 409133-67-1 409133-68-2 409133-69-3
409133-70-6 409133-71-7 409133-72-8 409133-73-9 409133-74-0
409133-75-1 409133-76-2 409133-77-3 409133-78-4 409133-79-5
409133-80-8 409133-81-9 409133-82-0 409400-81-3 409400-82-4
409400-83-5 409400-84-6 409400-85-7 409400-86-8 409400-87-9
409400-88-0
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65***

gene)
IT 330543-09-4, GenBank AJ310216 330543-10-7, GenBank AJ310217
330543-11-8, GenBank AJ310218 330543-12-9, GenBank AJ310219
330543-13-0, GenBank AJ310221 330543-14-1, GenBank AJ310223
330543-15-2, GenBank AJ310225 330543-16-3, GenBank AJ310226
330543-17-4, GenBank AJ310229 330543-18-5, GenBank AJ310230
330543-19-6, GenBank AJ310231 330543-20-9, GenBank AJ310232
330543-21-0, GenBank AJ310233 330543-22-1, GenBank AJ310236
330543-23-2, GenBank AJ310238 330777-51-0, GenBank AJ307630
330777-52-1, GenBank AJ307631 330777-53-2, GenBank AJ307632
330777-54-3, GenBank AJ307636 330777-55-4, GenBank AJ307640
330777-56-5, GenBank AJ307641 330777-57-6, GenBank AJ307643
330777-58-7, GenBank AJ307644 330777-59-8, GenBank AJ307645
330777-60-1, GenBank AJ307646 330777-61-2, GenBank AJ307647
330777-62-3, GenBank AJ307651 330777-63-4, GenBank AJ307652
330777-64-5, GenBank AJ307654 383716-71-0, GenBank AJ310215
383716-72-1, GenBank AJ310224 383716-73-2, GenBank AJ310228
383716-75-4, GenBank AJ310237 383716-76-5, GenBank AJ307637
383716-77-6, GenBank AJ307649 383716-78-7, GenBank AJ307653
384598-59-8, GenBank AJ310220 384598-71-4, GenBank AJ310234
384598-73-6, GenBank AJ310235 384598-75-8, GenBank AJ310239
384598-89-4, GenBank AJ307634 384598-91-8, GenBank AJ307635
384598-93-0, GenBank AJ307638 384598-95-2, GenBank AJ307639
384598-97-4, GenBank AJ307648 384598-99-6, GenBank AJ307650
385635-00-7, GenBank AJ310227 385635-02-9, GenBank AJ307642
385652-99-3, GenBank AJ310222 385653-01-0, GenBank AJ307633
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; ***identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism anal. of the ***hsp65*** gene)

L9 ANSWER 47 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:539667 CAPLUS <<LOGINID::20090617>>
DN 134:247672
TI A multiplex approach to molecular detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle
AU Sreevatsan, Srinand; Bookout, Jack B.; Ringpis, Fidel; Perumaalla, Veera S.; Ficht, Thomas A.; Adams, L. Garry; Hagius, Sue D.; Elzer, Philip H.; Bricker, Betsy J.; Kumar, Girish K.; Rajasekhar, M.; Isloor, Srikrishna; Barathur, Raj R.
CS ClinCyte, San Diego, CA, 92121, USA
SO Journal of Clinical Microbiology (2000), 38(7), 2602-2610
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB A multiplex amplification and detection platform for the ***diagnosis*** of ***Mycobacterium*** bovis and Brucella abortus infection simultaneously in bovine milk and nasal secretions was developed. This system (designated the bovine pathogen detection assay [BPDA]-PCR) consists of duplex amplification of species-specific targets (a region of the BCSP31K gene of B. abortus and a repeat-sequence region in the ***hsp65*** gene of M. bovis, resp.). This is followed by a solid-phase
probe capture hybridization of amplicons for detection. On the basis of spiking expts. with normal milk, the anal. sensitivity of the assay was

800 CFU equiv./mL of milk for B. abortus and as low as 4 CFU equiv. per mL of milk for M. bovis. BPDA-PCR was validated with 45 liver samples from lemmings exptl. infected with B. abortus. The assay sensitivity, based on culture status as a "gold std.," was 93.9%. In this expt., BPDA-PCR also ***identified*** five culture-neg. liver samples as pos. (41.7%). Field studies for the evaluation of BPDA-PCR were performed with samples from dairy animals from geog. distinct regions (India, Mexico, and Argentina). A high prevalence of shedding of B. abortus (samples from India) and M. bovis (samples from Mexico) was ***identified*** by BPDA-PCR. In samples from India, B. abortus shedding was ***identified*** in 86% of milk ring test-pos. animals (n = 15) and 80% of milk ring test-neg. cows (n = 5). In samples from Mexico, M. bovis was ***identified*** by PCR in 32.6% of pools (n = 46) of milk that each contained milk from 10 animals and in 56.2% of nasal swabs (n = 121) from cattle from tuberculin test-pos. herds. In contrast, the Argentine cattle (n = 70) had a modest prevalence of M. bovis shedding in nasal swabs (2.9%) and milk (1.4%) and of B. abortus in milk (11.4%). On the basis of these analyses, we ***identify*** BPDA-PCR as an optimal tool for both screening of herds and testing of individual animals in a disease eradication program. A combination of the duplex assay, screening of milk samples in pools, and the proposed algorithm provides a highly sensitive, cost-effective, and economically viable alternative to serol. testing.

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A multiplex approach to molecular detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle

AB A multiplex amplification and detection platform for the ***diagnosis*** of ***Mycobacterium*** bovis and Brucella abortus infection simultaneously in bovine milk and nasal secretions was developed. This system (designated the bovine pathogen. . . duplex amplification of species-specific targets (a region of the BCSP31K gene of B. abortus and a repeat-sequence region in the ***hsp65*** gene of M. bovis, resp.). This is followed by a solid-phase probe capture hybridization of amplicons for detection. On the. . . B. abortus. The assay sensitivity, based on culture status as a "gold std.," was 93.9%. In this expt., BPDA-PCR also ***identified*** five culture-neg. liver samples as pos. (41.7%). Field studies for the evaluation of BPDA-PCR were performed with samples from dairy. . . and Argentina). A high prevalence of shedding of B. abortus (samples from India) and M. bovis (samples from Mexico) was ***identified*** by BPDA-PCR. In samples from India, B. abortus shedding was ***identified*** in 86% of milk ring test-pos. animals (n = 15) and 80% of milk ring test-neg. cows (n = 5). In samples from Mexico, M. bovis was ***identified*** by PCR in 32.6% of pools (n = 46) of milk that each contained milk from 10 animals and in. . . nasal swabs (2.9%) and milk (1.4%) and of B. abortus in milk (11.4%). On the basis of these analyses, we ***identify*** BPDA-PCR as an optimal tool for both screening of herds and testing of individual animals in a disease eradication program.. . .

ST mol ***diagnosis*** BPDA PCR hybridization Brucella ***Mycobacterium*** infection cattle; bovine pathogen detection assay PCR hybridization Brucella ***Mycobacterium***

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(B. abortus BCSP31K gene and M. tuberculosis gene ***hsp65*** -specific ***primers*** ; multiplex approach (BPDA-PCR followed by

probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT Gene, microbial
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(BCSP31K; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, B. abortus BCSP31K gene and M. tuberculosis gene ***hsp65*** -specific ***primers*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT PCR (polymerase chain reaction)
(bovine pathogen detection assay [BPDA]-PCR; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle)

IT Gene, microbial
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle)

IT Brucella
(infection with, brucellosis; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle)

IT ***Diagnosis***
(mol.; multiplex approach (BPDA-PCR followed by probe capture hybridization) used in both screening of herds and individual animals for Brucella abortus and/or ***Mycobacterium*** bovis)

IT Milk
(multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT Brucella melitensis
Cattle
Mycobacterium bovis
Nucleic acid hybridization
Tuberculosis
(multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis infection in cattle)

IT DNA
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , B. abortus BCSP31K gene and M. tuberculosis gene ***hsp65*** -specific ***primers*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT Nose
(swab of; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or

Mycobacterium bovis in milk samples or nasal swabs)

IT 331290-67-6D, biotinylated 331290-68-7D, biotinylated
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(B. abortus BCSP31K gene-specific ***primer*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-69-8
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(B. abortus BCSP31K gene-specific probe; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-70-1D, biotinylated 331290-71-2D, biotinylated
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene ***hsp65*** M. tuberculosis complex-specific ***primer*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-72-3
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene ***hsp65*** M. tuberculosis complex-specific probe; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

L9 ANSWER 48 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:122970 CAPLUS <<LOGINID::20090617>>
DN 133:115654
TI Species ***identification*** of ***Mycobacterium*** avium complex isolates by a variety of molecular techniques
AU Beggs, Marjorie L.; Stevanova, Rossina; Eisenach, Kathleen D.
CS Department of Pathology, J. L. McClellan Memorial Veterans Hospital, University of Arkansas for Medical Sciences, Little Rock, AR, USA
SO Journal of Clinical Microbiology (2000), 38(2), 508-512
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Organisms in the ***Mycobacterium*** avium complex (MAC; M. avium, M. intracellulare, and "nonspecific or X" MAC) are emerging pathogens among individual organisms of which significant genetic variability is displayed. The objective of the present study was to evaluate various mol. methods for the rapid and definitive ***identification*** of MAC species. Isolates were obtained from both human immunodeficiency virus (HIV)-pos. patients and HIV-neg. patients with and without known predisposing conditions. The isolates were initially hybridized with nucleic acid probes complementary to the rRNA of the resp. ***mycobacterial*** species (AccuProbe Culture Confirmation kits for M. avium, M. intracellulare, and MAC species; Gen-Probe). Isolates were also examd. by PCR and in some cases by Southern blot hybridization for the insertion element IS1245. Two other techniques included a PCR assay that amplifies the mig gene, a putative virulence factor for MAC, and

hsp65 gene amplification and sequencing. This study led to the following observations. Eighty-five percent of the isolates from HIV-pos. patients were M. avium and 86% of the isolates from HIV-neg. patients were M. intracellulare. Fifteen of the M. avium isolates did not contain IS1245 and 7% of the M. intracellulare isolates were found to carry IS1245. All of the M. avium strains were mig pos., and all of the M. intracellulare strains were mig neg.

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Species ***identification*** of ***Mycobacterium*** avium complex isolates by a variety of molecular techniques

AB Organisms in the ***Mycobacterium*** avium complex (MAC; M. avium, M. intracellulare, and "nonspecific or X" MAC) are emerging pathogens among individual organisms of which. . . variability is displayed. The objective of the present study was to evaluate various mol. methods for the rapid and definitive ***identification*** of MAC species. Isolates were obtained from both human immunodeficiency virus (HIV)-pos. patients and HIV-neg. patients with and without known predisposing conditions. The isolates were initially hybridized with nucleic acid probes complementary to the rRNA of the resp. ***mycobacterial*** species (AccuProbe Culture Confirmation kits for M. avium, M. intracellulare, and MAC species; Gen-Probe). Isolates were also examd. by PCR. . . IS1245. Two other techniques included a PCR assay that amplifies the mig gene, a putative virulence factor for MAC, and ***hsp65*** gene amplification and sequencing. This study led to the following observations. Eighty-five percent of the isolates from HIV-pos. patients were. . .

ST ***Mycobacterium*** complex isolate ***identification*** PCR hybridization DNA sequence; HIV patient ***Mycobacterium*** isolate ***identification*** PCR hybridization DNA sequence

IT ***Primers*** (nucleic acid)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, gene mig-specific ***primers*** ; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Insertion sequence
RL: ANT (Analyte); ANST (Analytical study)
(IS1245; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(for 16S rRNA; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(***hsp65*** ; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(mig; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic

acid hybridization and DNA sequencing)

IT DNA
DNA
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , gene mig-specific ***primers*** ; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Human immunodeficiency virus
Mycobacterium avium
Mycobacterium intracellulare
Nucleic acid hybridization
PCR (polymerase chain reaction)
(species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT 285575-58-8
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene mig-specific lower ***primer*** ; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT 285575-57-7
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene mig-specific upper ***primer*** ; species ***identification*** of ***Mycobacterium*** avium complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

L9 ANSWER 49 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:782698 CAPLUS <<LOGINID::20090617>>
DN 132:190212
TI Discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction
AU Sircili, Marcelo Palma; Roxo, Eliana; Leao, Sylvia Cardoso
CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Sao Paulo, Escola Paulista de Medicina, Sao Paulo, CEP 04023-062, Brazil
SO Revista de Microbiologia (1999), 30(2), 144-148
CODEN: RMBGBP; ISSN: 0001-3714
PB Sociedade Brasileira de Microbiologia
DT Journal
LA English
AB ***Mycobacterium*** avium complex (MAC) species cannot be discriminated by the usual methods of biochem. ***identification*** of ***mycobacteria*** . This study showed that amplification by PCR of DT1 and DT6, two single copy sequences ***identified*** in the genome of M. avium serotype 2, the insertion sequence IS1245, found to be

consistently present in M. avium strains and the heat-shock protein gene ***hsp65*** , followed by restriction polymorphism anal., are rapid and accurate tests for the differentiation of the species M. avium, M. intracellulare, and M. scrofulaceum.

RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction

AB ***Mycobacterium*** avium complex (MAC) species cannot be discriminated by the usual methods of biochem. ***identification*** of ***mycobacteria*** . This study showed that amplification by PCR of DT1 and DT6, two single copy sequences ***identified*** in the genome of M. avium serotype 2, the insertion sequence IS1245, found to be consistently present in M. avium strains and the heat-shock protein gene ***hsp65*** , followed by restriction polymorphism anal., are rapid and accurate tests for the differentiation of the species M. avium, M. intracellulare,. . .

ST PCR ***identification*** ***Mycobacterium*** avium complex

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DT1; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DT6; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT Taxonomy
(Discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT Insertion sequence
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IS1245; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT ***Mycobacterium*** scrofulaceum
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT ***Mycobacterium*** avium
(member of MAC complex; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT ***Mycobacterium*** intracellulare
(member of the MAC complex; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 148908-89-8
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(AV6 PCR ***primer*** to DT6; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 148908-88-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(AV7 PCR ***primer*** to DT6; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 260042-37-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IN38 PCR ***primer*** to DT1; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 148909-28-8
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IN41 PCR ***primer*** to DT1; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 190977-48-1
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(P1 PCR ***primer*** to IS1245; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 260042-38-4
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(P2 PCR ***primer*** to IS1245; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 150951-89-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Tbl1 PCR ***primer*** for PRA; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)
IT 150951-90-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Tbl2 PCR ***primer*** for PRA; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

L9 ANSWER 50 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:595536 CAPLUS <<LOGINID::20090617>>
DN 132:118005
TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis
AU Wei, Cheng-Yu; Lee, Chun N.; Chu, Chin-Hwa; Hwang, Jiuan Jiuan; Lee, Chan Ping
CS Tzu Chi College of Medicine and Humanities, Tzu Chi General Hospital, Hualien, Taiwan
SO Kaohsiung Journal of Medical Sciences (1999), 15(7), 396-405
CODEN: KJMSFM; ISSN: 0257-5655
PB Kaohsiung Journal of Medical Sciences
DT Journal
LA English
AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four M. tuberculosis isolates, four M. bovis BCG isolates, and one of each for M. fortuitum, M. avium, M. intracellulare, M. szulgai, M.

scrofulaceum, M. chelonei, and M. gordonae from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR. The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of only M. tuberculosis and M. bovis BCG. Furthermore, targeting the mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA. When the mtp40 genomic fragment was used as the target DNA, the sensitivity of detection was 10 copies of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid from the patient with tuberculous meningitis.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis

AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four M. tuberculosis isolates, four M. bovis BCG isolates, and one of each for M. fortuitum, M. avium,. . . M. scrofulaceum, M. chelonei, and M. gordonae from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR. The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of only M. tuberculosis and M. bovis BCG. Furthermore, targeting the. . . mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA.. . . of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid. . .

ST PCR ***Mycobacterium*** tuberculosis detection IS6110 mtp40 ***hsp65***

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65, gene for; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT Insertion sequence
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(IS6110; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium***

tuberculosis)
IT ***Mycobacterium*** tuberculosis
PCR (polymerase chain reaction)
(detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)
IT ***Diagnosis***
(mol.; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(mtp40; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)
IT 256216-29-2 256216-30-5 256216-31-6 256216-32-7
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** for IS6110; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)
IT 256216-33-8 256216-34-9 256216-35-0 256216-36-1
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(PCR ***primer*** for mtp40; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

L9 ANSWER 51 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:436334 CAPLUS <<LOGINID::20090617>>
DN 131:253056
TI Characterization to species level of clinical isolates of the ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme analysis
AU Garriga, Xavier; Cortes, Pilar; March, Francesca; Rodriguez, Purificacion; Garrigo, Montserrat; Moreno, Carmen; Garcia, Elena; Coll, Pere; Prats, Guillem
CS Servei de Microbiologia, Hospital de la Santa Creu i Sant Pau, Barcelona, 08025, Spain
SO Clinical Microbiology and Infection (1999), 5(6), 379-382
CODEN: CMINFM; ISSN: 1198-743X
PB Decker Europe
DT Journal
LA English
AB The AccuProbe System was used to classify clin. isolates of M. avium and M. intracellulare. ***Primers*** were used to amplify specific DNA fragments (DT1-DT6) for ***identification*** of these isolates by PCR. In addn., PCR-restriction enzyme anal. (PRA) was performed on these strains based on ***primers*** amplifying a fragment of the gene ***hsp65*** . PRA was more sensitive than the AccuProbe System and DT1-DT6 amplification.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Characterization to species level of clinical isolates of the ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme analysis

AB The AccuProbe System was used to classify clin. isolates of M. avium and M. intracellulare. ***Primers*** were used to amplify specific DNA fragments (DT1-DT6) for ***identification*** of these isolates by PCR. In addn., PCR-restriction enzyme anal. (PRA) was performed on these strains based on ***primers*** amplifying a fragment of the gene ***hsp65*** . PRA was more sensitive than the AccuProbe System and DT1-DT6 amplification.

ST ***Mycobacterium*** ***diagnosis*** probe restriction enzyme PCR

IT Nucleic acid hybridization
(DNA-DNA; characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Heat-shock proteins
RL: ADV (Adverse effect, including toxicity); ARU (Analytical role, unclassified); ANST (Analytical study); BIOL (Biological study)
(HSP 65; characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT ***Diagnosis***
Mycobacterium avium
Mycobacterium intracellulare
PCR (polymerase chain reaction)
(characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT Gene, microbial
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(***hsp65*** ; characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII 148908-88-7, DNA, d(C-G-T-T-C-G-A-T-C-G-C-A-G-T-T-T-G-T-G-C-A-G-C-G-C-G-T-A-C-A) 148908-89-8, DNA, d(A-T-G-G-C-C-G-G-G-A-G-A-C-G-A-T-C-T-A-T-G-C-C-G-G-C-G-T-A-C) 150951-89-6 150951-90-9
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(characterization to species level of clin. isolates of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and PCR-restriction enzyme anal.)

L9 ANSWER 52 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1999:370904 CAPLUS <<LOGINID::20090617>>

DN 131:180372

TI Species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene

AU Rastogi, Nalin; Goh, Khye Seng; Berchel, Mylene
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, Pointe a Pitre, 97165, Guadeloupe
SO Journal of Clinical Microbiology (1999), 37(6), 2016-2019
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB PCR-restriction fragment length polymorphism anal. (PRA) of the ***hsp65*** gene present in all ***mycobacteria*** was used in the present investigation to characterize ***Mycobacterium*** leprae. Bacilli were extd. and purified from different organs from exptl. infected armadillos and nude mice (Swiss mice of nu/nu origin). A total of 15 samples were assayed in duplicate, and the results were compared with those obtained for a total of 147 cultivable ***mycobacteria*** representing 34 species. Irresp. of its origin or viability, M. leprae strains from all the samples were uniformly characterized by two fragments of 315 and 135 bp upon BstEII digestion and two fragments of 265 and 130 bp upon HaeIII digestion. PRA is a relatively simple method and permits the conclusive ***identification*** of M. leprae to the species level.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene
AB PCR-restriction fragment length polymorphism anal. (PRA) of the ***hsp65*** gene present in all ***mycobacteria*** was used in the present investigation to characterize ***Mycobacterium*** leprae. Bacilli were extd. and purified from different organs from exptl. infected armadillos and nude mice (Swiss mice of nu/nu. . . 15 samples were assayed in duplicate, and the results were compared with those obtained for a total of 147 cultivable ***mycobacteria*** representing 34 species. Irresp. of its origin or viability, M. leprae strains from all the samples were uniformly characterized by. . . two fragments of 265 and 130 bp upon HaeIII digestion. PRA is a relatively simple method and permits the conclusive ***identification*** of M. leprae to the species level.
ST PCR RFLP ***Mycobacterium*** species ***identification*** ***hsp65***
IT ***Primers*** (nucleic acid)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(***hsp65*** ; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT DNA
DNA
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES

(Uses)
(***primer*** ; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT DNA sequences
(***primers*** ; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT ***Mycobacterium*** leprae
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT 150951-89-6
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of useful ***primer*** Tb11; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT 150951-90-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence of useful ***primer*** Tb12; species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)
IT 81295-18-3 93229-61-9, Restriction endonuclease bsteii
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(species-specific ***identification*** of ***Mycobacterium*** leprae by PCR-restriction fragment length polymorphism anal. of ***hsp65*** gene)

L9 ANSWER 53 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:200588 CAPLUS <<LOGINID::20090617>>
DN 131:68708
TI Polymerase chain reaction, with sequencing, as a ***diagnostic*** tool in culture-negative bacterial meningitis
AU Dicuonzo, Giordano; Lorino, Giulia; Lilli, Daniela; Rivanera, Daniela; Guarino, Paola; Angeletti, Silvia; Gherardi, Giovanni; Filadoro, Francesco
CS Libera Universita, Campus Bio-Medico, Facolta Medicina e Chirurgia, Universita "La Sapienza", Rome, 83-00155, Italy
SO Clinical Microbiology and Infection (1999), 5(2), 92-96
CODEN: CMINFM; ISSN: 1198-743X
PB Decker Europe
DT Journal
LA English
AB To evaluate the feasibility of using 16S rDNA universal ***primer*** PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium*** tuberculosis protein gene PCR as a method to det. a bacterial etiol. in culture-neg. cerebrospinal fluid (CSF) samples. One hundred and forty-nine CSF samples from 128 patients were processed. DNA was extd.

from the CSF samples and amplified with the eubacterial 16S rDNA ***primers*** P11E and P13B, and with the 65-kDa heat shock protein gene ***mycobacterial*** ***primers*** . The amplicons were ***identified*** by sequencing and specific oligoprobe hybridization. Overall, a microbiol. ***diagnosis*** was made in 11 of 125 ultimately culture-neg. cases. The use of 65-kDa heat shock protein gene PCR was needed to improve the ***diagnosis*** of tuberculous meningitis; in four patients, prospectively studied, the outcome of antituberculous therapy could also be followed. In culture-neg. bacterial meningitis it is possible to improve the microbiol. ***diagnosis*** by use of 16S rDNA amplification and sequencing, together with amplification of a more specific gene in ***mycobacteria*** .

RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Polymerase chain reaction, with sequencing, as a ***diagnostic*** tool in culture-negative bacterial meningitis

AB To evaluate the feasibility of using 16S rDNA universal ***primer*** PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium*** tuberculosis protein gene PCR as a method to det. a bacterial etiol. in culture-neg. cerebrospinal fluid (CSF) samples. One hundred. . . samples from 128 patients were processed. DNA was extd. from the CSF samples and amplified with the eubacterial 16S rDNA ***primers*** P11E and P13B, and with the 65-kDa heat shock protein gene ***mycobacterial*** ***primers*** . The amplicons were ***identified*** by sequencing and specific oligoprobe hybridization. Overall, a microbiol. ***diagnosis*** was made in 11 of 125 ultimately culture-neg. cases. The use of 65-kDa heat shock protein gene PCR was needed to improve the ***diagnosis*** of tuberculous meningitis; in four patients, prospectively studied, the outcome of antituberculous therapy could also be followed. In culture-neg. bacterial meningitis it is possible to improve the microbiol. ***diagnosis*** by use of 16S rDNA amplification and sequencing, together with amplification of a more specific gene in ***mycobacteria*** .

ST PCR 16S rDNA ***HSP65*** ***diagnosis*** tuberculous meningitis

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)

IT ***Primers*** (nucleic acid)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 65; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)

IT Gene, animal
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***HSP65*** ; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis***

of culture-neg. tuberculous meningitis in humans)
IT ***Mycobacterium*** tuberculosis
PCR (polymerase chain reaction)
(PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)
IT ***Diagnosis***
(mol.; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)
IT DNA
DNA
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)
IT DNA
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rDNA, 16 S; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)
IT Meningitis
(tuberculous; PCR using 16S rDNA and ***HSP65*** protein ***primers*** of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg. tuberculous meningitis in humans)

L9 ANSWER 54 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:173164 CAPLUS <<LOGINID::20090617>>
DN 131:68653
TI ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***
AU Ringuet, H.; Akoua-Koffi, C.; Honore, S.; Varnerot, A.; Vincent, V.; Berche, P.; Gaillard, J. L.; Pierre-Audigier, C.
CS Service de Microbiologie, Hopital Necker-Enfants Malades, Paris, 75015, Fr.
SO Journal of Clinical Microbiology (1999), 37(3), 852-857
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Partial sequencing of the ***hsp65*** gene was used for the ***identification*** of rapidly growing ***mycobacteria*** (RGM).
A
441-bp fragment (A. Telenti, F. Marchesi, M. Balz, F. Bally, E. Bottger, and T. Bodmer, J. Clin. Microbiol. 31:175-178, 1993) was amplified and sequenced by an automated fluorescence-based method involving capillary electrophoresis. Type strains of 10 RGM species were first studied. Each species had a unique nucleotide sequence, distinguishing it clearly from the other species. A panel of strains from the four main RGM species responsible for human infections, ***Mycobacterium*** abscessus, ***Mycobacterium*** chelonae, ***Mycobacterium*** fortuitum, and ***Mycobacterium*** peregrinum, was also studied. There were few sequence differences within each of these species (<2% of bases were different from the type strain sequence), and they had no effect on species assignment. ***Hsp65*** sequencing unambiguously

differentiated M. chelonae and M. abscessus, two species difficult to ***identify*** by classical methods and 16S rRNA gene sequencing. The devised procedure is a rapid and reliable tool for the ***identification*** of RGM species.

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***

AB Partial sequencing of the ***hsp65*** gene was used for the ***identification*** of rapidly growing ***mycobacteria*** (RGM). A
441-bp fragment (A. Telenti, F. Marchesi, M. Balz, F. Bally, E. Bottger, and T. Bodmer, J. Clin. Microbiol.. . . it clearly from the other species. A panel of strains from the four main RGM species responsible for human infections, ***Mycobacterium*** abscessus, ***Mycobacterium*** chelonae, ***Mycobacterium*** fortuitum, and ***Mycobacterium*** peregrinum, was also studied. There were few sequence differences within each of these species (<2% of bases were different from the type strain sequence), and they had no effect on species assignment. ***Hsp65*** sequencing unambiguously differentiated M. chelonae and M. abscessus, two species difficult to ***identify*** by classical methods and 16S rRNA gene sequencing. The devised procedure is a rapid and reliable tool for the ***identification*** of RGM species.

ST ***Mycobacterium*** species ***identification*** sequencing ***hsp65*** gene

IT DNA sequence analysis
DNA sequences
Mycobacterium
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium fortuitum
Mycobacterium peregrinum
PCR (polymerase chain reaction)
(***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***)

IT Gene, microbial
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(***hsp65*** ; ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***)

IT 228573-12-4
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** Tb11; ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***)

IT 228573-13-5
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** Tb12; ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***)

IT 224287-13-2 224287-18-7 225760-17-8 229016-49-3 229016-50-6 229016-51-7 229016-52-8 229016-53-9 229016-54-0 229016-56-2 229016-57-3
RL: ANT (Analyte); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; ***hsp65*** Sequencing for ***identification*** of rapidly growing ***mycobacteria***)

L9 ANSWER 55 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:723093 CAPLUS <<LOGINID::20090617>>
DN 128:30784
OREF 128:5933a,5936a
TI Rapid ***identification*** of ***mycobacteria*** to species level by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene and proposition of an algorithm to differentiate 34 ***mycobacterial*** species
AU Devallois, Anne; Goh, Khye Seng; Rastogi, Nalin
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, Pointe a Pitre, 97165, Guadeloupe
SO Journal of Clinical Microbiology (1997), 35(11), 2969-2973
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB PCR-restriction fragment length polymorphism anal. (PRA) of the ***hsp65*** gene was applied to 108 ***mycobacterial*** isolates representing 34 species to evaluate its potential as a rapid ref. method. A total of 49 distinct patterns were obtained; 25 species were characterized by a single PRA pattern, while 9 species gave more than one specific pattern. An algorithm describing these 34 species (which includes five addnl. species and new subgroups of ***Mycobacterium*** kansasii, M. abscessus, and M. peregrinum) is proposed. A relatively simple and inexpensive method, PRA may be particularly helpful in routine clin. microbiol. labs.
TI Rapid ***identification*** of ***mycobacteria*** to species level by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene and proposition of an algorithm to differentiate 34 ***mycobacterial*** species
AB PCR-restriction fragment length polymorphism anal. (PRA) of the ***hsp65*** gene was applied to 108 ***mycobacterial*** isolates representing 34 species to evaluate its potential as a rapid ref. method. A total of 49 distinct patterns were. . . more than one specific pattern. An algorithm describing these 34 species (which includes five addnl. species and new subgroups of ***Mycobacterium*** kansasii, M. abscessus, and M. peregrinum) is proposed. A relatively simple and inexpensive method, PRA may be particularly helpful in. . .
ST PCR RFLP ***identification*** taxonomy ***Mycobacterium***
IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(***hsp65*** ; ***identification*** of ***mycobacteria*** to species level by ***hsp65*** gene PCR-RFLP proposal of algorithm differentiating 34 ***mycobacterial*** species)
IT ***Mycobacterium***
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
Taxonomy
(***identification*** of ***mycobacteria*** to species level by ***hsp65*** gene PCR-RFLP proposal of algorithm differentiating 34 ***mycobacterial*** species)
IT 150951-89-6 150951-90-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** Tb11; ***identification*** of

mycobacteria to species level by ***hsp65*** gene PCR-RFLP proposal of algorithm differentiating 34 ***mycobacterial*** species)

L9 ANSWER 56 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:36419 CAPLUS <<LOGINID::20090617>>
DN 126:70783
OREF 126:13605a,13608a
TI ***Identification*** and subspecific differentiation of ***Mycobacterium*** scrofulaceum by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein
AU Swanson, Douglas S.; Pan, Xi; Musser, James M.
CS Section of Infectious Diseases, Department of Pediatrics, Baylor College of Medicine, Houston, TX, 77030, USA
SO Journal of Clinical Microbiology (1996), 34(12), 3151-3159
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB ***Mycobacterium*** scrofulaceum is most commonly recovered from children with cervical lymphadenitis, although it also accounts for approx. 2% of the ***mycobacterial*** infections in AIDS patients. Species assignment of M. scrofulaceum isolates by conventional techniques can be difficult and time-consuming. To develop a strategy for rapid species assignment of these organisms, a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein in 37 isolates from diverse sources was sequenced. Eight ***hsp65*** alleles were ***identified*** , and these sequences formed phylogenetic clusters and lineages largely distinct from other ***Mycobacterium*** species. There was incomplete correlation between serovar designation and ***hsp65*** allele assignment. The ***hsp65*** data correlated strongly with the results of sequence anal. of the gene coding for 16S rRNA. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene provides a rapid and unambiguous method for species assignment of these acid-fast organisms for ***diagnostic*** purposes.
TI ***Identification*** and subspecific differentiation of ***Mycobacterium*** scrofulaceum by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein
AB ***Mycobacterium*** scrofulaceum is most commonly recovered from children with cervical lymphadenitis, although it also accounts for approx. 2% of the ***mycobacterial*** infections in AIDS patients. Species assignment of M. scrofulaceum isolates by conventional techniques can be difficult and time-consuming. To develop a strategy for rapid species assignment of these organisms, a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein in 37 isolates from diverse sources was sequenced. Eight ***hsp65*** alleles were ***identified*** , and these sequences formed phylogenetic clusters and lineages largely distinct from other ***Mycobacterium*** species. There was incomplete correlation between serovar designation and ***hsp65*** allele assignment. The ***hsp65*** data correlated strongly with the results of sequence anal. of the gene coding for 16S rRNA. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene provides a rapid and unambiguous method for species assignment of these acid-fast organisms for ***diagnostic*** purposes.
ST sequencing gene ***hsp65*** typing taxonomy ***Mycobacterium*** ; ***diagnosis*** ***Mycobacterium*** gene ***hsp65*** sequencing
IT Gene, microbial

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(***hsp65*** ; ***identification*** and differentiation of ***Mycobacterium*** scrofulaceum by automated sequencing gene ***hsp65*** region encoding 65-kDa heat shock protein)

IT DNA sequence analysis
DNA sequences
Mycobacterium scrofulaceum
Protein sequences
Taxonomy
(***identification*** and differentiation of ***Mycobacterium*** scrofulaceum by automated sequencing gene ***hsp65*** region encoding 65-kDa heat shock protein)

IT 150951-89-6 150951-90-9
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; ***identification*** and differentiation of ***Mycobacterium*** scrofulaceum by automated sequencing gene ***hsp65*** region encoding 65-kDa heat shock protein)

L9 ANSWER 57 OF 71 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights reserved on STN

AN 2007263708 EMBASE <<LOGINID::20090617>>

TI Application of restriction enzyme analysis technique based on 65kDa heat shock protein gene for fingerprinting and differentiation of ***Mycobacterium*** tuberculosis clinical strains isolated from tuberculosis patients in Ahwaz, Iran.

AU Khosravi, Azar D., Dr. (correspondence); Hashemi, Abdulrazagh
CS Dept. of Microbiology, School of Medicine, Ahwaz Jondi Shapour University of Medical Sciences, Ahwaz, Iran, Islamic Republic of. khosraviaz@yahoo.com

SO Pakistan Journal of Medical Sciences, (Apr 2007) Vol. 23, No. 2, pp. 216-219.
Refs: 14
ISSN: 1682-024X CODEN: PJMSC6
CY Pakistan
DT Journal; Article
FS 015 Chest Diseases, Thoracic Surgery and Tuberculosis
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LA English
SL English
ED Entered STN: 21 Jun 2007
Last Updated on STN: 21 Jun 2007

AB Objective: Application of ***identification*** methodology of restriction enzyme analysis (REA) for fingerprinting of the expanded population of ***Mycobacterium*** tuberculosis (MTB) isolates. Methodology: A total of 150 clinical isolates from patients referred to TB reference laboratory, Public Health Centre, Ahwaz, Iran, were ***identified*** as MTB by using conventional culture and biochemical tests from January to December 2004. The PCR-REA method uses a PCR step based on amplification of a 439 bp fragment of ***hsp65*** gene involving genus specific ***primers*** and restriction enzyme analysis by digestion of products with HaeIII & BstEII enzymes were employed. Results: The identical restriction patterns similar to MTB reference strains equal to 160/145/72bp fragments for Hae III and 250/120/82bp fragments for Bst EII digests were seen in 145 isolates (96.6%). The diverse patterns were observed for five isolates in Hae III digest as

180/100/80 bp, 194/72 bp and 160/145 bp representing the possible intra-species variation within studied MTB strains , while their Bst EII digestion patterns showed no variation. Conclusions: The PCR-REA technique revealed three different new patterns for Hae III digest. However to verify that they are indeed MTB isolates, a sequence-based analysis of the exceptional isolates should be performed.

TI Application of restriction enzyme analysis technique based on 65kDa heat shock protein gene for fingerprinting and differentiation of ***Mycobacterium*** tuberculosis clinical strains isolated from tuberculosis patients in Ahwaz, Iran.

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CT Medical Descriptors:
adult
aged
article
bacterial strain
bacterium culture
bacterium isolate
biochemistry
controlled study
*DNA fingerprinting
DNA sequence
female
genetic variability
human
intraspecific variation
Iran
laboratory
*lung tuberculosis: ET, etiology
male
****Mycobacterium tuberculosis***
nonhuman
*polymerase chain reaction
*restriction mapping
*tuberculosis: ET, etiology
*heat shock protein 65

L9 ANSWER 58 OF 71 MEDLINE on STN
AN 2008153624 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 18310283
TI A novel vaccine targeting gastrin-releasing peptide: efficient inhibition of breast cancer growth in vivo.
AU Guojun Wu; Wei Guo; Kedong Ouyan; Yi He; Yanfei Xie; Qingmei Chen; Yankai Zhang; Jie Wu; Hao Fan; Taiming Li; Jingjing Liu; Rongyue Cao
CS Minigene Pharmacy Laboratory of the Biopharmaceutical College, China Pharmaceutical University, Nanjing, PR China.
SO Endocrine-related cancer, (2008 Mar) Vol. 15, No. 1, pp. 149-59.

Journal code: 9436481. ISSN: 1351-0088.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200805
ED Entered STN: 4 Mar 2008
Last Updated on STN: 9 May 2008
Entered Medline: 8 May 2008
AB Gastrin-releasing peptide (GRP), a bombesin-like peptide, is an autocrine growth factor that can stimulate the growth of various cancer cells. We developed a novel protein vaccine ***HSP65*** -(GRP-10)(6) (HG6) that consists of six copies of a 10-amino acid residue epitope of GRP C-terminal fragment carried by ***mycobacterial*** 65 kDa ***HSP65*** and then immunized mice via subcutaneous injection. Strong humoral and cell-mediated immune responses were induced. High titer of anti-GRP antibodies was detected in immunized mice sera by ELISA and verified by Western blot analysis. Activity of CD4+T lymphocytes, especially high levels of interferon (INF)-gamma, were developed in mice immunized with HG6 when compared with ***HSP65*** or PBS. We found that immunogene tumor therapy with a vaccine based on GRP was effective at both protective and therapeutic antitumor immunity in breast tumor models in mice. The purified GRP monoclonal antibody (McAb) was proved to be potential in inhibiting EMT-6 tumor cell proliferation in vitro. The attenuation induced by active immune responses on tumor-induced angiogenesis was observed with an intradermal tumor model in mice. Taken together, we demonstrate for the first time that immune responses that are elicited by a novel chimeric protein vaccine targeting GRP can suppress the proliferation of breast tumor cell EMT-6 in mice, and it may be of importance in the further exploration of the applications of other autocrine growth factor ***identified*** in human and other animal in cancer therapy.
AB . . . is an autocrine growth factor that can stimulate the growth of various cancer cells. We developed a novel protein vaccine ***HSP65*** -(GRP-10)(6) (HG6) that consists of six copies of a 10-amino acid residue epitope of GRP C-terminal fragment carried by ***mycobacterial*** 65 kDa ***HSP65*** and then immunized mice via subcutaneous injection. Strong humoral and cell-mediated immune responses were induced. High titer of anti-GRP antibodies. . . Activity of CD4+T lymphocytes, especially high levels of interferon (INF)-gamma, were developed in mice immunized with HG6 when compared with ***HSP65*** or PBS. We found that immunogene tumor therapy with a vaccine based on GRP was effective at both protective and. . . in mice, and it may be of importance in the further exploration of the applications of other autocrine growth factor ***identified*** in human and other animal in cancer therapy.
CT . . . Breast Neoplasms: PA, pathology
*Breast Neoplasms: TH, therapy
CD4-Positive T-Lymphocytes: IM, immunology
*Cancer Vaccines: AD, administration & dosage
Cell Proliferation
*** DNA Primers***
Enzyme-Linked Immunosorbent Assay
Immunization
Interferon-gamma: ME, metabolism
Lymphocyte Activation
Mice

Mice, Inbred BALB C
Neovascularization, Pathologic
*Peptide Fragments:. . .
CN 0 (Antibodies, Monoclonal); 0 (Cancer Vaccines); 0 (DNA ***Primers***); 0 (Peptide Fragments); 0 (Recombinant Fusion Proteins)

L9 ANSWER 59 OF 71 MEDLINE on STN
AN 2007352566 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 17449684
TI Diversity of environmental ***Mycobacterium*** isolates from hemodialysis water as shown by a multigene sequencing approach.
AU Gomila Margarita; Ramirez Antonio; Lalucat Jorge
CS Area Microbiologia, Departament de Biologia, Universitat de les Illes Balears, Campus UIB, Crtra. Valldemosa km 7.5, Facultad de Ciencias, 07122 Palma de Mallorca, and Servei de Microbiologia, Hospital Universitari Son Dureta, Illes Baleares, Spain.
SO Applied and environmental microbiology, (2007 Jun) Vol. 73, No. 12, pp. 3787-97. Electronic Publication: 2007-04-20.
Journal code: 7605801. ISSN: 0099-2240.
Report No.: NLM-PMC1932725.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
OS GENBANK-AM421246; GENBANK-AM421247; GENBANK-AM421248; GENBANK-AM421249; GENBANK-AM421250; GENBANK-AM421251; GENBANK-AM421252; GENBANK-AM421253; GENBANK-AM421254; GENBANK-AM421255; GENBANK-AM421256; GENBANK-AM421257; GENBANK-AM421258; GENBANK-AM421259; GENBANK-AM421260; GENBANK-AM421261; GENBANK-AM421262; GENBANK-AM421263; GENBANK-AM421264; GENBANK-AM421265; GENBANK-AM421266; GENBANK-AM421267; GENBANK-AM421268; GENBANK-AM421269; GENBANK-AM421270; GENBANK-AM421271; GENBANK-AM421272; GENBANK-AM421273; GENBANK-AM421274; GENBANK-AM421275; GENBANK-AM421276; GENBANK-AM421277; GENBANK-AM421278; GENBANK-AM421279; GENBANK-AM421280; GENBANK-AM421281; GENBANK-AM421282; GENBANK-AM421283; GENBANK-AM421284; GENBANK-AM421285; GENBANK-AM421286; GENBANK-AM421287; GENBANK-AM421288; GENBANK-AM421289; GENBANK-AM421290; GENBANK-AM421291; GENBANK-AM421292; GENBANK-AM421293; GENBANK-AM421294; GENBANK-AM421295; GENBANK-AM421296; GENBANK-AM421297; GENBANK-AM421298; GENBANK-AM421299; GENBANK-AM421300; GENBANK-AM421301; GENBANK-AM421302; GENBANK-AM421303; GENBANK-AM421304; GENBANK-AM421305; GENBANK-AM421306; GENBANK-AM421307; GENBANK-AM421308; GENBANK-AM421309; GENBANK-AM421310; GENBANK-AM421311; GENBANK-AM421312; GENBANK-AM421313; GENBANK-AM421314; GENBANK-AM421315; GENBANK-AM421316; GENBANK-AM421317; GENBANK-AM421318; GENBANK-AM421319; GENBANK-AM421320; GENBANK-AM421321; GENBANK-AM421322; GENBANK-AM421323; GENBANK-AM421324; GENBANK-AM421325; GENBANK-AM421326; GENBANK-AM421327; GENBANK-AM421328; GENBANK-AM421329; GENBANK-AM421330; GENBANK-AM421331; GENBANK-AM421332; GENBANK-AM421333; GENBANK-AM421334; GENBANK-AM421335; GENBANK-AM421336; GENBANK-AM421337; GENBANK-AM421338; GENBANK-AM421339; GENBANK-AM421340; GENBANK-AM421341; GENBANK-AM421342; GENBANK-AM421343; GENBANK-AM421344; GENBANK-AM421345; GENBANK-AM421346; GENBANK-AM421347; GENBANK-AM421348; GENBANK-AM421349; GENBANK-AM421350; GENBANK-AM421351; GENBANK-AM421352; GENBANK-AM421353; GENBANK-AM421354; GENBANK-AM421355; GENBANK-AM421356; GENBANK-AM421357; GENBANK-AM421358; GENBANK-AM421359; GENBANK-AM421360; GENBANK-AM421361; GENBANK-AM421362; GENBANK-AM421363; GENBANK-AM421364; GENBANK-AM421365; GENBANK-AM421366; GENBANK-AM421367; GENBANK-AM421368; GENBANK-AM421369;

GENBANK-AM421370; GENBANK-AM421371; GENBANK-AM421372; GENBANK-AM421373;
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GENBANK-AM421386; GENBANK-AM421387; GENBANK-AM421388; GENBANK-AM421389;
GENBANK-AM421390; GENBANK-AM421391; GENBANK-AM421392; GENBANK-AM421393;
GENBANK-AM421394; GENBANK-AM421395; GENBANK-AM421396; GENBANK-AM421397;
GENBANK-AM421398; GENBANK-AM421399; GENBANK-AM421400; GENBANK-AM421401;
GENBANK-AM421402; GENBANK-AM421403; GENBANK-AM421404; GENBANK-AM421405;
GENBANK-AM421406; GENBANK-AM421407; GENBANK-AM421408; GENBANK-AM421409;
GENBANK-AM421410; GENBANK-AM421411; GENBANK-AM421412; GENBANK-AM421413;
GENBANK-AM421414; GENBANK-AM421415; GENBANK-AM421416; GENBANK-AM421417;
GENBANK-AM421418; GENBANK-AM421419; GENBANK-AM421420; GENBANK-AM421421;
GENBANK-AM421422; GENBANK-AM421423; GENBANK-AM421424; GENBANK-AM421425;
GENBANK-AM421426; GENBANK-AM421427; GENBANK-AM421428; GENBANK-AM421429;
GENBANK-AM501932

EM 200803

ED Entered STN: 15 Jun 2007
Last Updated on STN: 7 Mar 2008
Entered Medline: 6 Mar 2008

AB Here we used a multigene sequencing approach for the ***identification*** and molecular typing of environmental ***mycobacteria*** of the fast-growing subgroup. Strains were isolated from hemodialysis water and clinical samples. Eleven type strains of related species of the genus were also included in this study. To gain further insight into the diversity of the environmental ***mycobacteria*** , we analyzed several housekeeping genes (16S rRNA, ITS1, gyrB, ***hsp65*** , recA, rpoB, and sodA). No individual phylogenetic tree allowed good discrimination of all of the species studied. However, a concatenated and a consensus analysis, combining the genes, allowed better discrimination of each strain to the species level, and the increase in sequence size also led to greater tree robustness. This approach is useful not only for the discrimination and ***identification*** of environmental ***mycobacteria*** but also for their molecular typing and studies of population genetics. Our results demonstrate high genetic diversity among the isolates obtained, which are probably new species of the genus.

TI Diversity of environmental ***Mycobacterium*** isolates from hemodialysis water as shown by a multigene sequencing approach.

AB Here we used a multigene sequencing approach for the ***identification*** and molecular typing of environmental ***mycobacteria*** of the fast-growing subgroup. Strains were isolated from hemodialysis water and clinical samples. Eleven type strains of related species of the genus were also included in this study. To gain further insight into the diversity of the environmental ***mycobacteria*** , we analyzed several housekeeping genes (16S rRNA, ITS1, gyrB, ***hsp65*** , recA, rpoB, and sodA). No individual phylogenetic tree allowed good discrimination of all of the species studied. However, a concatenated. . . increase in sequence size also led to greater tree robustness. This approach is useful not only for the discrimination and ***identification*** of environmental ***mycobacteria*** but also for their molecular typing and studies of population genetics. Our results demonstrate high genetic diversity among the isolates. . .

CT Base Sequence
Cluster Analysis
*** DNA Primers: GE, genetics***

*Genes, Bacterial: GE, genetics
*Genetic Variation
*Hemodialysis Solutions: AN, analysis
Molecular Sequence Data
****Mycobacterium: GE, genetics***
*Phylogeny
*Sequence Analysis, DNA: MT, methods
Sputum: MI, microbiology
CN 0 (DNA ***Primers***); 0 (Hemodialysis Solutions)

L9 ANSWER 60 OF 71 MEDLINE on STN
AN 2007174460 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 17373188
TI ***Identification*** of novel ***hsp65*** RFLPs for ***Mycobacterium*** leprae.
AU Martiniuk Frank; Tambini Marc; Rahimian Joseph; Moreira Andre; Yee Herman; Tchou-Wong Kam-Meng; Hanna Bruce A; Rom William N; Levis William R
CS Department of Medicine-Pulmonary Division, New York University School of Medicine, New York, NY 10016, USA.. martif02@med.nyu.edu
NC M01 RR00096 (United States NCRR NIH HHS)
SO Journal of drugs in dermatology : JDD, (2007 Mar) Vol. 6, No. 3, pp. 268-74.
Journal code: 101160020. ISSN: 1545-9616.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
LA English
FS Priority Journals
EM 200704
ED Entered STN: 24 Mar 2007
Last Updated on STN: 24 Apr 2007
Entered Medline: 23 Apr 2007
AB Leprosy or Hansen's disease is a chronic infectious disease caused by an acid-fast bacillus, ***Mycobacterium*** leprae (M. leprae). The bacilli proliferate in macrophages infiltrating the skin and gain entry to the dermal nerves via the laminar surface of Schwann cells where they replicate. After entry, the Schwann cells proliferate and then die. Conclusive ***identification*** of M. leprae DNA in a sample can be obtained by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) for the heat shock 65 gene (***hsp65***). Molecular epidemiology will make it possible to study the global distributions of M. leprae, explore the relationship between genotypes-incidence rates, mode of transmission, and the type of disease (tuberculoid vs. lepromatous). We amplified DNA using PCR for the ***hsp65*** gene from 24 skin lesions from patients ***diagnosed*** with various types of leprosy. Fifteen out of 24 were positive for the ***hsp65*** gene. Digestion with HaeIII-PAGE for the RFLP confirmation of the presence of M. leprae DNA showed the typical pattern in 5 out of 24 and 2 novel patterns in 10 out of 24 patients. We confirmed the presence of M. leprae DNA by sequencing the genes for gyraseA or B and folP, which contained only M. leprae specific single nucleotide polymorphisms (SNPs). Thus, we describe novel ***hsp65*** RFLPs for M. leprae found in a high frequency making them ideal for future epidemiology and transmission studies.
TI ***Identification*** of novel ***hsp65*** RFLPs for ***Mycobacterium*** leprae.
AB Leprosy or Hansen's disease is a chronic infectious disease caused by an

acid-fast bacillus, ***Mycobacterium*** leprae (M. leprae). The bacilli proliferate in macrophages infiltrating the skin and gain entry to the dermal nerves via the laminar surface of Schwann cells where they replicate. After entry, the Schwann cells proliferate and then die. Conclusive ***identification*** of M. leprae DNA in a sample can be obtained by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) for the heat shock 65 gene (***hsp65***). Molecular epidemiology will make it possible to study the global distributions of M. leprae, explore the relationship between genotypes-incidence rates, mode of transmission, and the type of disease (tuberculoid vs. lepromatous). We amplified DNA using PCR for the ***hsp65*** gene from 24 skin lesions from patients ***diagnosed*** with various types of leprosy. Fifteen out of 24 were positive for the ***hsp65*** gene. Digestion with HaeIII-PAGE for the RFLP confirmation of the presence of M. leprae DNA showed the typical pattern in. . . for gyraseA or B and folP, which contained only M. leprae specific single nucleotide polymorphisms (SNPs). Thus, we describe novel ***hsp65*** RFLPs for M. leprae found in a high frequency making them ideal for future epidemiology and transmission studies.

CT *Bacterial Proteins: GE, genetics
*Chaperonins: GE, genetics
DNA Gyrase: GE, genetics
*** DNA Primers***
DNA, Bacterial: CH, chemistry
DNA, Bacterial: GE, genetics
Electrophoresis, Polyacrylamide Gel
Epidemiology, Molecular
Gene Frequency
Humans
Leprosy: MI, microbiology
****Mycobacterium leprae: GE, genetics***
Paraffin Embedding
Polymorphism, Restriction Fragment Length

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***); EC 5.99.1.- (DNA Gyrase)

L9 ANSWER 61 OF 71 MEDLINE on STN
AN 2007168555 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 17369945
TI ***Identification*** of ***mycobacteria*** of the MAIS Complex and M. tuberculosis by restriction fragment length polymorphism analysis of ***hsp65*** gene.
AU Krasnova M A; Makarova M V; Skotnikova O I; Moroz A M
CS Moscow Municipal Scientific and Practical Center for Struggle against Tuberculosis, Moscow Department of Health.
SO Bulletin of experimental biology and medicine, (2006 Aug) Vol. 142, No. 2, pp. 222-5.
Journal code: 0372557. ISSN: 0007-4888.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
LA English; Russian
FS Priority Journals
EM 200704
ED Entered STN: 20 Mar 2007
Last Updated on STN: 28 Apr 2007

Entered Medline: 27 Apr 2007
AB Restriction fragment length polymorphism analysis of ***hsp65*** gene was performed on museum strains of ***mycobacteria*** using Hin6I restrictase. Study of restriction profiles allowed us to distinguish ***mycobacterial*** species of the MAIS complex and several strains of nontuberculous ***mycobacteria*** .
TI ***Identification*** of ***mycobacteria*** of the MAIS Complex and M. tuberculosis by restriction fragment length polymorphism analysis of ***hsp65*** gene.
AB Restriction fragment length polymorphism analysis of ***hsp65*** gene was performed on museum strains of ***mycobacteria*** using Hin6I restrictase. Study of restriction profiles allowed us to distinguish ***mycobacterial*** species of the MAIS complex and several strains of nontuberculous ***mycobacteria*** .
CT *Bacterial Proteins: GE, genetics
*Chaperonins: GE, genetics
*** DNA Primers***
Electrophoresis, Agar Gel
****Mycobacterium: GE, genetics***
Polymorphism, Restriction Fragment Length
Species Specificity
CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 62 OF 71 MEDLINE on STN
AN 2006053996 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 16438154
TI Evaluation of polymerase chain reaction and restriction enzyme analysis for routine ***identification*** of ***mycobacteria*** : accuracy, rapidity, and cost analysis.
AU Prammananan Therdsak; Cheunoy Wattana; Na-Ubol Preeyawit; Tingtoy Nipa; Srimuang Somboon; Chaiprasert Angkana
CS Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, Bangkok, Thailand.
SO The Southeast Asian journal of tropical medicine and public health, (2005 Sep) Vol. 36, No. 5, pp. 1252-60.
Journal code: 0266303. ISSN: 0125-1562.
CY Thailand
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200603
ED Entered STN: 28 Jan 2006
Last Updated on STN: 1 Apr 2006
Entered Medline: 31 Mar 2006
AB Polymerase chain reaction and restriction enzyme analysis (PCR-REA) of the ***hsp65*** gene was evaluated for use as a routine ***identification*** method for ***identifying*** ***mycobacteria*** . The accuracy, rapidity, and cost were assessed compared with the conventional biochemical method. Five hundred and forty-one ***mycobacterial*** clinical isolates obtained from the Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, were submitted for PCR-REA and biochemical ***identification*** . PCR-REA showed high concordant result with 100, 96.2, and 94.1% for ***identification*** of ***Mycobacterium***

tuberculosis, rapid- and slow-growing ***mycobacteria*** , respectively. Discordant results were obtained from 24 (4.4%) out of 541 isolates, consisting of 9 rapid growers (6 M. chelonae, 2 M. abscessus, and 1 M. fortuitum) and 15 slow growers (9 M. scrofulaceum, 2 M. gordonae, 1 M. avium, 1 M. kansasii, 1 M. malmoense, and 1 M. terrae complex). PCR-REA demonstrated not only accurate results but was also less expensive (2.1 US dollars/sample). This method was rapid with a turn-around time of 30 hours compared with 2-4 weeks for the conventional method.

TI Evaluation of polymerase chain reaction and restriction enzyme analysis for routine ***identification*** of ***mycobacteria*** : accuracy, rapidity, and cost analysis.

AB Polymerase chain reaction and restriction enzyme analysis (PCR-REA) of the ***hsp65*** gene was evaluated for use as a routine ***identification*** method for ***identifying*** ***mycobacteria*** . The accuracy, rapidity, and cost were assessed compared with the conventional biochemical method. Five hundred and forty-one ***mycobacterial*** clinical isolates obtained from the Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, were submitted for PCR-REA and biochemical ***identification*** . PCR-REA showed high concordant result with 100, 96.2, and 94.1% for ***identification*** of ***Mycobacterium*** tuberculosis, rapid- and slow-growing ***mycobacteria*** , respectively. Discordant results were obtained from 24 (4.4%) out of 541 isolates, consisting of 9 rapid growers (6 M. chelonae,. . .

CT Bacterial Proteins: IP, isolation & purification
Base Sequence
Chaperonins: IP, isolation & purification
Costs and Cost Analysis
*** DNA Primers***
DNA, Bacterial
Humans
*** Mycobacterium: CL, classification***
*** Mycobacterium: GE, genetics***
****Mycobacterium: IP, isolation & purification***
*Polymerase Chain Reaction
Reproducibility of Results
*Restriction Mapping
Thailand

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 63 OF 71 MEDLINE on STN
AN 2005651342 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 16332331
TI Occurrence and characterization of multiple novel genotypes of ***Mycobacterium*** immunogenum and ***Mycobacterium*** chelonae in metalworking fluids.
AU Khan Izhar U H; Selvaraju Suresh B; Yadav Jagjit S
CS Environmental Genetics and Molecular Toxicology Division, Department of Environmental Health, University of Cincinnati Medical Center, Cincinnati, OH 45267-0056, USA.
NC 1R01OH007364 (United States NIOSH CDC HHS)
SO FEMS microbiology ecology, (2005 Nov 1) Vol. 54, No. 3, pp. 329-38. Journal code: 8901229. ISSN: 0168-6496.
CY Netherlands
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)

(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
EM 200606
ED Entered STN: 16 Dec 2005
Last Updated on STN: 16 Jun 2006
Entered Medline: 15 Jun 2006
AB Rapidly growing ***mycobacteria*** colonize metalworking fluids, leading to contamination of occupational environments and exposure-related respiratory illnesses in machine workers. Lately, it has been emphasized that these fluids are colonizable by a single genotype of a rapidly growing ***mycobacterium*** species, ***Mycobacterium*** immunogenum. Here, we report on the genotypic diversity of ***mycobacteria*** in these fluids, including isolation and characterization of multiple novel genotypes of two distinct species, ***Mycobacterium*** chelonae and M. immunogenum. Using agar culturing and ***Mycobacterium*** -specific PCR, 13 ***mycobacterial*** isolates were recovered from 100 geographically diverse in-use metalworking fluid samples. Based on restriction fragment length polymorphism of PCR products, DNA sequencing (***hsp65*** gene segment), and phylogenetic analysis of 16S-23S rDNA internal transcribed spacer (ITS) sequences, six isolates were ***identified*** as M. immunogenum and seven as M. chelonae; an additional isolate from metalworking fluid diluent water was ***identified*** as M. diernhoferi. Genomic DNA macro-restriction fragment pattern analysis, using pulsed-field gel electrophoresis with XbaI and SpeI restriction digestions, showed intraspecies variation among the isolates of M. immunogenum and M. chelonae. Visual and computer-assisted dendrogram analysis of the XbaI macro-restriction patterns revealed three novel genotypes of M. immunogenum and two of M. chelonae, whereas SpeI macro-restriction patterns revealed only two genotypes for each isolate. None of the ***identified*** genotypes matched the reportedly dominant one of M. immunogenum from metalworking fluids. Both ***mycobacterial*** species are prevalent in metalworking fluids and there is a considerable strain-level genetic diversity within them.
TI Occurrence and characterization of multiple novel genotypes of ***Mycobacterium*** immunogenum and ***Mycobacterium*** chelonae in metalworking fluids.
AB Rapidly growing ***mycobacteria*** colonize metalworking fluids, leading to contamination of occupational environments and exposure-related respiratory illnesses in machine workers. Lately, it has been emphasized that these fluids are colonizable by a single genotype of a rapidly growing ***mycobacterium*** species, ***Mycobacterium*** immunogenum. Here, we report on the genotypic diversity of ***mycobacteria*** in these fluids, including isolation and characterization of multiple novel genotypes of two distinct species, ***Mycobacterium*** chelonae and M. immunogenum. Using agar culturing and ***Mycobacterium*** -specific PCR, 13 ***mycobacterial*** isolates were recovered from 100 geographically diverse in-use metalworking fluid samples. Based on restriction fragment length polymorphism of PCR products, DNA sequencing (***hsp65*** gene segment), and phylogenetic analysis of 16S-23S rDNA internal transcribed spacer (ITS) sequences, six isolates were ***identified*** as M. immunogenum and seven as M. chelonae; an additional isolate from metalworking fluid diluent water was ***identified*** as M. diernhoferi. Genomic DNA macro-restriction fragment pattern analysis, using pulsed-field gel electrophoresis with XbaI and SpeI restriction

digestions, showed. . . immunogenum and two of M. chelonae, whereas SpeI macro-restriction patterns revealed only two genotypes for each isolate. None of the ***identified*** genotypes matched the reportedly dominant one of M. immunogenum from metalworking fluids. Both ***mycobacterial*** species are prevalent in metalworking fluids and there is a considerable strain-level genetic diversity within them.

CT Bacterial Proteins: GE, genetics
Base Sequence
Chaperonins: GE, genetics
Cluster Analysis
*** DNA Primers***
DNA, Ribosomal: GE, genetics
Electrophoresis, Gel, Pulsed-Field
Genotype
*Metallurgy
Molecular Sequence Data
****Mycobacterium: GE, genetics***
*Occupational Exposure
*Phylogeny
Polymorphism, Restriction Fragment Length
Sequence Analysis, DNA
Species Specificity
*Water Microbiology

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Ribosomal); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 64 OF 71 MEDLINE on STN
AN 2001092058 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 11090265
TI Description of a novel ***Mycobacterium*** simiae allelic variant isolated from Caribbean AIDS patients by PCR-restriction enzyme analysis and sequencing of ***hsp65*** gene.
AU Legrand E; Goh K S; Sola C; Rastogi N
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, BP 484, F-97165 Pointe a Pitre-Cedex, Guadeloupe.
SO Molecular and cellular probes, (2000 Dec) Vol. 14, No. 6, pp. 355-63. Journal code: 8709751. ISSN: 0890-8508.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200101
ED Entered STN: 22 Mar 2001
Last Updated on STN: 22 Mar 2001
Entered Medline: 25 Jan 2001
AB A sudden upsurge in the isolation of ***Mycobacterium*** simiae from terminally ill AIDS patients was recently reported on the Caribbean island of Guadeloupe. ***Identification*** of these M. simiae isolates was achieved using biochemical tests and further confirmed by PCR-restriction analysis (PRA) of a 439-bp fragment of ***hsp65*** . A novel PRA profile III (three Bst EII fragments of 240/125/80 bp and four Hae III fragments of 145/125/40/25 bp) was observed in four blood isolates from two patients. The 16 S rRNA gene sequencing of the hypervariable A region confirmed that all the pattern III isolates were indeed M. simiae species, and the ***hsp65*** sequencing confirmed the existence of a new ***hsp65*** allele in these caribbean isolates. A ***hsp65***

sequence-based phylogenetic tree was also created for 39 species including M. simiae and related ***mycobacterial*** species as well as other rapid and slow growing ***mycobacteria*** , and may serve as an useful tool for ***identification*** of ***mycobacteria*** to species level.

TI Description of a novel ***Mycobacterium*** simiae allelic variant isolated from Caribbean AIDS patients by PCR-restriction enzyme analysis and sequencing of ***hsp65*** gene.

AB A sudden upsurge in the isolation of ***Mycobacterium*** simiae from terminally ill AIDS patients was recently reported on the Caribbean island of Guadeloupe. ***Identification*** of these M. simiae isolates was achieved using biochemical tests and further confirmed by PCR-restriction analysis (PRA) of a 439-bp fragment of ***hsp65*** . A novel PRA profile III (three Bst EII fragments of 240/125/80 bp and four Hae III fragments of 145/125/40/25 bp). . . sequencing of the hypervariable A region confirmed that all the pattern III isolates were indeed M. simiae species, and the ***hsp65*** sequencing confirmed the existence of a new ***hsp65*** allele in these caribbean isolates. A ***hsp65*** sequence-based phylogenetic tree was also created for 39 species including M. simiae and related ***mycobacterial*** species as well as other rapid and slow growing ***mycobacteria*** , and may serve as an useful tool for ***identification*** of ***mycobacteria*** to species level.

CT . . .
Immunodeficiency Syndrome: MI, microbiology
Adult
Aged
Alleles
*Bacterial Proteins
Base Sequence
*Chaperonins: GE, genetics
DNA: AN, analysis
DNA: BL, blood
*** DNA Primers: CH, chemistry***
*DNA, Bacterial: AN, analysis
DNA, Ribosomal: GE, genetics
*Genetic Variation
Genome, Bacterial
Guadeloupe: EP, epidemiology
Humans
Middle Aged
Molecular Sequence Data
****Mycobacterium: IP, isolation & purification***
*** Mycobacterium Infections: EP, epidemiology***
*** Mycobacterium Infections: GE, genetics***
****Mycobacterium Infections: MI, microbiology***
Phylogeny
*Polymerase Chain Reaction: MT, methods
*Restriction Mapping: MT, methods
Sequence Alignment
Sequence Homology, Nucleic Acid

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 65 OF 71 MEDLINE on STN
AN 1998010213 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 9350730
TI Molecular characterization of ***Mycobacterium*** avium complex isolates giving discordant results in AccuProbe tests by PCR-restriction enzyme analysis, 16S rRNA gene sequencing, and DT1-DT6 PCR.
AU Devallois A; Picardeau M; Paramasivan C N; Vincent V; Rastogi N
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, Pointe-a-Pitre, Guadeloupe, French West Indies.
SO Journal of clinical microbiology, (1997 Nov) Vol. 35, No. 11, pp. 2767-72.
Journal code: 7505564. ISSN: 0095-1137.
Report No.: NLM-PMC230058.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 199802
ED Entered STN: 17 Feb 1998
Last Updated on STN: 17 Feb 1998
Entered Medline: 3 Feb 1998
AB Based on cultural and biochemical tests, a total of 84 strains (72 clinical and 12 environmental isolates from the Caribbean Isles, Europe, and the Indian subcontinent) were ***identified*** as members of the ***Mycobacterium*** avium complex (MAC). They were further characterized with MAC, M. avium, and M. intracellulare probes of the AccuProbe system, and this was followed by selective amplification of DT6 and DT1 sequences. Seventy isolates gave concordant results; 63 were ***identified*** as M. avium, 5 were ***identified*** as M. intracellulare, and 24 remained untypeable by both methods. Fourteen isolates gave discrepant results, as they were DT1 positive but gave negative results by the M. intracellulare AccuProbe test. Consequently, a detailed molecular analysis of all DT1-positive isolates (14 discrepant strains plus 5 M. intracellulare strains) was performed by PCR-restriction analysis (PRA) of the ***hsp65*** gene and 16S rRNA gene sequencing. The results confirmed the reported heterogeneity of M. intracellulare, as only 6 of 19 isolates (32%) gave PRA results compatible with published M. intracellulare profiles while the rest of the isolates were grouped in four previously unpublished profiles. 16S rRNA gene sequencing showed that only 8 of 19 isolates (42%) were related to M. intracellulare IWGMT 90247 (EMBL accession no. X88917), the rest being related to MCRO19 (EMBL accession no. X93030) and MIWGTMR10 (EMBL accession no. X88915). In conclusion, we have characterized a significant number of MAC isolates which were not ***identified*** by the AccuProbe test, PRA, or 16S rRNA sequencing. However, all of them were ***identifiable*** by DT1-DT6 PCR (they were DT6 negative and DT1 positive) and could be tentatively ***identified*** as M. intracellulare based on previously published observations. It is noteworthy that the majority of such isolates (14 of 19) were from the Indian subcontinent, with 12 of 14 being environmental isolates. Our study confirms the marked heterogeneity of M. intracellulare isolates and shows the utility of in-house DT1 PCR to detect this group of isolates, which would otherwise have been missed by the AccuProbe system in a routine clinical microbiology laboratory.
TI Molecular characterization of ***Mycobacterium*** avium complex isolates giving discordant results in AccuProbe tests by PCR-restriction enzyme analysis, 16S rRNA gene sequencing, and DT1-DT6 PCR.. . .

AB . . . total of 84 strains (72 clinical and 12 environmental isolates from the Caribbean Isles, Europe, and the Indian subcontinent) were ***identified*** as members of the ***Mycobacterium*** avium complex (MAC). They were further characterized with MAC, M. avium, and M. intracellulare probes of the AccuProbe system, and this was followed by selective amplification of DT6 and DT1 sequences. Seventy isolates gave concordant results; 63 were ***identified*** as M. avium, 5 were ***identified*** as M. intracellulare, and 24 remained untypeable by both methods. Fourteen isolates gave discrepant results, as they were DT1 positive. . . . of all DT1-positive isolates (14 discrepant strains plus 5 M. intracellulare strains) was performed by PCR-restriction analysis (PRA) of the ***hsp65*** gene and 16S rRNA gene sequencing. The results confirmed the reported heterogeneity of M. intracellulare, as only 6 of 19. . . and MIWGTMR10 (EMBL accession no. X88915). In conclusion, we have characterized a significant number of MAC isolates which were not ***identified*** by the AccuProbe test, PRA, or 16S rRNA sequencing. However, all of them were ***identifiable*** by DT1-DT6 PCR (they were DT6 negative and DT1 positive) and could be tentatively ***identified*** as M. intracellulare based on previously published observations. It is noteworthy that the majority of such isolates (14 of 19). . .

CT Base Sequence
*** DNA Primers***
DNA, Bacterial: GE, genetics
*DNA, Ribosomal: GE, genetics
Europe
Genetic Variation
Guadeloupe
Humans
India
Molecular Sequence Data
*** Mycobacterium avium Complex: CL, classification***
****Mycobacterium avium Complex: GE, genetics***
****Mycobacterium avium Complex: IP, isolation & purification***
****Mycobacterium avium-intracellulare Infection: DI, diagnosis***
*Polymerase Chain Reaction: MT, methods
*RNA, Ribosomal, 16S: GE, genetics
*** Reagent Kits, Diagnostic***
Sequence Alignment
Sequence Homology, Nucleic Acid

CN 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (RNA, Ribosomal, 16S); 0 (Reagent Kits, ***Diagnostic***)

L9 ANSWER 66 OF 71 MEDLINE on STN
AN 1997424502 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 9278615
TI Routine rapid ***Mycobacterium*** species assignment based on species-specific allelic variation in the 65-kilodalton heat shock protein gene (***hsp65***).
AU Pai S; Esen N; Pan X; Musser J M
CS Clinical Microbiology Laboratory, Methodist Hospital Houston, Tex, USA.
NC DA-09238 (United States NIDA NIH HHS)
SO Archives of pathology & laboratory medicine, (1997 Aug) Vol. 121, No. 8, pp. 859-64.
Journal code: 7607091. ISSN: 0003-9985.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199709
ED Entered STN: 8 Oct 1997
Last Updated on STN: 3 Mar 2000
Entered Medline: 19 Sep 1997
AB OBJECTIVE: To assess the utility of automated DNA sequencing strategies for ***Mycobacterium*** species assignment and surrogate rifampin susceptibility testing of ***Mycobacterium*** tuberculosis complex isolates in a hospital-based clinical microbiology laboratory. DESIGN: Consecutive patient specimens (n = 161) cultured in BACTEC 12B medium (growth index of 50 or greater) or on solid media (Lowenstein-Jensen) were analyzed. A 360-bp segment of a gene (***hsp65***) encoding a 65-kd heat shock protein was sequenced to ***identify*** species-specific allelic polymorphism. ***Identification*** of sequence variation in the rpoB gene encoding the beta subunit of RNA polymerase was used as a surrogate method to assess rifampin susceptibility in M tuberculosis complex isolates. RESULTS: The automated DNA sequencing strategies rapidly ***identified*** virtually all ***mycobacteria*** (158 [98%] of 161) to the species level and unambiguously characterized the region of rpoB that contains mutations responsible for rifampin resistance in M tuberculosis strains. With few exceptions, DNA sequence-based species assignment data agreed with ***diagnostic*** information obtained by conventional methods. All discrepancies were due to ambiguous biochemical test data or interpretation. The rifampin susceptibility phenotype was correctly predicted for all strains by rpoB sequencing. CONCLUSIONS: Rapid ***mycobacterial*** species assignment based on ***hsp65*** sequencing can be routinely performed in a hospital ***diagnostic*** microbiology laboratory setting. The method is especially useful for ***identification*** of fastidious organisms, such as ***Mycobacterium*** genavense. Sequencing of the rifampin-resistance-determining region of rpoB provides a convenient surrogate strategy for predicting rifampin susceptibility in M tuberculosis complex isolates.
TI Routine rapid ***Mycobacterium*** species assignment based on species-specific allelic variation in the 65-kilodalton heat shock protein gene (***hsp65***).
AB OBJECTIVE: To assess the utility of automated DNA sequencing strategies for ***Mycobacterium*** species assignment and surrogate rifampin susceptibility testing of ***Mycobacterium*** tuberculosis complex isolates in a hospital-based clinical microbiology laboratory. DESIGN: Consecutive patient specimens (n = 161) cultured in BACTEC 12B. . . medium (growth index of 50 or greater) or on solid media (Lowenstein-Jensen) were analyzed. A 360-bp segment of a gene (***hsp65***) encoding a 65-kd heat shock protein was sequenced to ***identify*** species-specific allelic polymorphism. ***Identification*** of sequence variation in the rpoB gene encoding the beta subunit of RNA polymerase was used as a surrogate method to assess rifampin susceptibility in M tuberculosis complex isolates. RESULTS: The automated DNA sequencing strategies rapidly ***identified*** virtually all ***mycobacteria*** (158 [98%] of 161) to the species level and unambiguously characterized the region of rpoB that contains mutations responsible for rifampin resistance in M tuberculosis strains. With few exceptions, DNA sequence-based species assignment data agreed with

diagnostic information obtained by conventional methods. All discrepancies were due to ambiguous biochemical test data or interpretation. The rifampin susceptibility phenotype was correctly predicted for all strains by rpoB sequencing. CONCLUSIONS: Rapid ***mycobacterial*** species assignment based on ***hsp65*** sequencing can be routinely performed in a hospital ***diagnostic*** microbiology laboratory setting. The method is especially useful for ***identification*** of fastidious organisms, such as ***Mycobacterium*** genavense. Sequencing of the rifampin-resistance-determining region of rpoB provides a convenient surrogate strategy for predicting rifampin susceptibility in M tuberculosis. . .

CT Alleles
*Bacterial Proteins: GE, genetics
Bacterial Typing Techniques
*Chaperonins: GE, genetics
*** DNA Primers: CH, chemistry***
*DNA, Bacterial: AN, analysis
DNA-Directed RNA Polymerases: GE, genetics
Humans
Microbial Sensitivity Tests
****Mycobacterium: CL, classification***
*** Mycobacterium: GE, genetics***
*** Mycobacterium: IP, isolation & purification***
*** Mycobacterium tuberculosis: DE, drug effects***
*** Mycobacterium tuberculosis: GE, genetics***
*** Mycobacterium tuberculosis: IP, isolation & purification***
Polymerase Chain Reaction
Rifampin: PD, pharmacology
Sequence Analysis, DNA: MT, methods

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***); EC 2.7.7.6 (DNA-Directed RNA Polymerases); EC 2.7.7.6 (RNA polymerase beta subunit)

L9 ANSWER 67 OF 71 MEDLINE on STN
AN 1997256941 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 9103645
TI ***Mycobacterium*** mageritense sp. nov.
AU Domenech P; Jimenez M S; Menendez M C; Bull T J; Samper S; Manrique A; Garcia M J
CS Departamento de Medicina Preventiva, Facultad de Medicina, Universidad Autonoma de madrid, Spain.
SO International journal of systematic bacteriology, (1997 Apr) Vol. 47, No. 2, pp. 535-40.
Journal code: 0042143. ISSN: 0020-7713.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
OS GENBANK-M29558; GENBANK-M29566; GENBANK-M29567; GENBANK-M59056; GENBANK-U77305; GENBANK-U86083; GENBANK-U86084; GENBANK-U86085; GENBANK-U86086; GENBANK-U86087; GENBANK-U86088; GENBANK-U86089; GENBANK-X52861; GENBANK-X52921; GENBANK-X52922; GENBANK-X52933; GENBANK-X55599; GENBANK-X58890; GENBANK-X65528; GENBANK-X65529;

GENBANK-X80771; GENBANK-X81385; GENBANK-X81392; GENBANK-X82235; GENBANK-X82236; GENBANK-X86082; GENBANK-X99838; GENBANK-Z48211; GENBANK-Z48214; GENBANK-Z48216; +

EM 199706

ED Entered STN: 12 Jun 1997
Last Updated on STN: 12 Jun 1997
Entered Medline: 3 Jun 1997

AB Strains of a new species of rapidly growing, nonphotochromogenic ***mycobacteria*** , ***Mycobacterium*** mageritense, were isolated from human sputum. The growth characteristics, acid fastness, and mycolic acids of the isolates were consistent with those of ***Mycobacterium*** species. The isolates were ***identified*** as members of a new species by performing a biochemical analysis and DNA-DNA hybridization experiments, and by comparing the sequences of several conserved genes, such as the 16S rRNA, ***hsp65*** , and sodA genes. A phylogenetic analysis in which 16S rRNA and sodA sequences were used ***identified*** M. mageritense as a novel distinct species and placed M. mageritense between members of the ***Mycobacterium*** fortuitum complex and the thermotolerant rapidly growing group. Our results demonstrate that the taxonomic value of sodA sequence analysis in the genus ***Mycobacterium*** is similar to the well-established value of 16S rRNA sequence analysis.

TI ***Mycobacterium*** mageritense sp. nov.

AB Strains of a new species of rapidly growing, nonphotochromogenic ***mycobacteria*** , ***Mycobacterium*** mageritense, were isolated from human sputum. The growth characteristics, acid fastness, and mycolic acids of the isolates were consistent with those of ***Mycobacterium*** species. The isolates were ***identified*** as members of a new species by performing a biochemical analysis and DNA-DNA hybridization experiments, and by comparing the sequences of several conserved genes, such as the 16S rRNA, ***hsp65*** , and sodA genes. A phylogenetic analysis in which 16S rRNA and sodA sequences were used ***identified*** M. mageritense as a novel distinct species and placed M. mageritense between members of the ***Mycobacterium*** fortuitum complex and the thermotolerant rapidly growing group. Our results demonstrate that the taxonomic value of sodA sequence analysis in the genus ***Mycobacterium*** is similar to the well-established value of 16S rRNA sequence analysis.

CT Bacterial Proteins: GE, genetics
Base Sequence
*** DNA Primers: GE, genetics***
DNA, Bacterial: GE, genetics
Genes, Bacterial
Humans
Molecular Sequence Data
****Mycobacterium: CL, classification***
*** Mycobacterium: GE, genetics***
*** Mycobacterium: IP, isolation & purification***
Phylogeny
Polymerase Chain Reaction
Polymorphism, Restriction Fragment Length
RNA, Bacterial: GE, genetics
RNA, Ribosomal, 16S:. . .

CN 0 (Bacterial Proteins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S); 0 (SodA protein, Bacteria); EC

1.15.1.1 (Superoxide Dismutase)

L9 ANSWER 68 OF 71 MEDLINE on STN
AN 1997256926 MEDLINE <<LOGINID::20090617>>
DN PubMed ID: 9103630
TI Subspecific differentiation of ***Mycobacterium*** avium complex strains by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein.
AU Swanson D S; Kapur V; Stockbauer K; Pan X; Frothingham R; Musser J M
CS Department of Pediatrics, Baylor College of Medicine, Houston, Texas 77030, USA.
NC AI07392 (United States NIAID NIH HHS)
AI37004 (United States NIAID NIH HHS)
DA09238 (United States NIDA NIH HHS)
+
SO International journal of systematic bacteriology, (1997 Apr) Vol. 47, No. 2, pp. 414-9.
Journal code: 0042143. ISSN: 0020-7713.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
OS GENBANK-U85631; GENBANK-U85632; GENBANK-U85633; GENBANK-U85634; GENBANK-U85635; GENBANK-U85636; GENBANK-U85637; GENBANK-U85638; GENBANK-U85639; GENBANK-U85640; GENBANK-U85641
EM 199706
ED Entered STN: 12 Jun 1997
Last Updated on STN: 29 Jan 1999
Entered Medline: 3 Jun 1997
AB To develop a strategy for rapid species assignment and strain differentiation of ***Mycobacterium*** avium complex (MAC) organisms, the sequence of a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein was determined for 56 isolates, including 21 patient isolates and 35 reference strains. Eleven ***hsp65*** alleles were ***identified*** , and there was no sharing of alleles between strains classified as M. avium and ***Mycobacterium*** intracellulare based on serovar and species-specific DNA hybridization probes. Phylogenetic analysis showed that 30 strains had one of two ***hsp65*** alleles which were found in known M. avium organisms, 23 strains had one of six alleles allied with known M. intracellulare organisms, and three MAC isolates had one of three ***hsp65*** alleles that differed substantially from the consensus M. avium and M. intracellulare ***hsp65*** sequences. Estimates of strain relationships based on the sequences of ***hsp65*** and the 16S-23S ribosomal DNA internal transcribed spacer were similar. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene from MAC organisms provides a rapid and unambiguous marker system for strain differentiation and permits specific assignment of these acid-fast organisms for ***diagnostic*** purposes.
TI Subspecific differentiation of ***Mycobacterium*** avium complex strains by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein.
AB To develop a strategy for rapid species assignment and strain differentiation of ***Mycobacterium*** avium complex (MAC) organisms,

the sequence of a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein was determined for 56 isolates, including 21 patient isolates and 35 reference strains. Eleven ***hsp65*** alleles were ***identified*** , and there was no sharing of alleles between strains classified as M. avium and ***Mycobacterium*** intracellulare based on serovar and species-specific DNA hybridization probes. Phylogenetic analysis showed that 30 strains had one of two ***hsp65*** alleles which were found in known M. avium organisms, 23 strains had one of six alleles allied with known M. intracellulare organisms, and three MAC isolates had one of three ***hsp65*** alleles that differed substantially from the consensus M. avium and M. intracellulare ***hsp65*** sequences. Estimates of strain relationships based on the sequences of ***hsp65*** and the 16S-23S ribosomal DNA internal transcribed spacer were similar. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene from MAC organisms provides a rapid and unambiguous marker system for strain differentiation and permits specific assignment of these acid-fast organisms for ***diagnostic*** purposes.

CT Alleles
*Bacterial Proteins
Base Sequence
*Chaperonins: GE, genetics
*** DNA Primers: GE, genetics***
DNA, Bacterial: GE, genetics
DNA, Ribosomal: GE, genetics
*Genes, Bacterial
Humans
Molecular Sequence Data
****Mycobacterium avium Complex: CL, classification***
****Mycobacterium avium Complex: GE, genetics***
*** Mycobacterium avium Complex: IP, isolation & purification***
Phylogeny
Polymorphism, Genetic
RNA, Bacterial: GE, genetics
RNA, Ribosomal, 16S: GE, genetics
RNA,. . .

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S); 0 (RNA, Ribosomal, 23S); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 69 OF 71 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2005:974796 SCISEARCH <<LOGINID::20090617>>
GA The Genuine Article (R) Number: 966LD
TI Method for rapid ***identification*** and differentiation of the species of the ***Mycobacterium*** chelonae complex based on 16S-23S rRNA gene internal transcribed Spacer PCR-restriction analysis
AU Yadav J S (Reprint)
CS Univ Cincinnati, Med Ctr, Dept Environm Hlth, Environm Genet & Mol Toxicol Div, Cincinnati, OH 45267 USA (Reprint)
AU Khan I U H; Selvaraju S B
CS E-mail: Jagjit.Yadav@uc.edu
CYA USA
SO JOURNAL OF CLINICAL MICROBIOLOGY, (SEP 2005) Vol. 43, No. 9, pp. 4466-4472.
ISSN: 0095-1137.
PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.

DT Article; Journal
LA English
REC Reference Count: 26
ED Entered STN: 6 Oct 2005
Last Updated on STN: 6 Oct 2005
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Members of the ***Mycobacterium*** chelonae complex (MCC), including M. immunogenum, M. chelonae, and M. abscessus, have been associated with nosocomial infections and occupational hypersensitivity pneumonitis due to metalworking fluid (MWF) exposures. In order to minimize these health hazards, an effective and rapid assay for detection of MCC species and differentiation of MCC species from other species of rapidly growing ***mycobacteria*** (RGM) and from one another is warranted. Here we report such a method, based on the variable 16S-23S rRNA gene internal transcribed spacer (ITS) region. ***Mycobacterium*** genus-specific ***primers*** derived from highly conserved sequences in the ITS region and the flanking 16S rRNA gene were used. Specificity of the ***primers*** was verified using the MCC member species, 11 non-MCC RGM species, 3 slow-growing ***mycobacterial*** (SGM) species (two strains each), and 19 field isolates, including 18 MCC isolates (from in-use MWF) and one non-MCC isolate (from reverse osmosis water). The ITS amplicon size of M. immunogenum varied from those of M. chelonae and M. abscessus. Sequencing of the similar to 250-bp-long ITS amplicons of the three MCC member species showed differences in 24 to 34 bases, thereby yielding variable deduced restriction maps. ITS PCR-restriction analysis using the in silico-selected restriction enzyme MaeII or HphI differentiated the three MCC members from one another and from other RGM and SGM species without sequencing. The enzyme MaeII discriminated all three member species; however, HphI could only differentiate M. immunogenum from M. chelonae and M. abscessus. Use of an optimized rapid DNA template preparation step based on direct cell lysis in the PCR tube added to the simplicity and adaptability of the developed assay.

TI Method for rapid ***identification*** and differentiation of the species of the ***Mycobacterium*** chelonae complex based on 16S-23S rRNA gene internal transcribed Spacer PCR-restriction analysis

AB Members of the ***Mycobacterium*** chelonae complex (MCC), including M. immunogenum, M. chelonae, and M. abscessus, have been associated with nosocomial infections and occupational hypersensitivity. . . effective and rapid assay for detection of MCC species and differentiation of MCC species from other species of rapidly growing ***mycobacteria*** (RGM) and from one another is warranted. Here we report such a method, based on the variable 16S-23S rRNA gene internal transcribed spacer (ITS) region. ***Mycobacterium*** genus-specific ***primers*** derived from highly conserved sequences in the ITS region and the flanking 16S rRNA gene were used. Specificity of the ***primers*** was verified using the MCC member species, 11 non-MCC RGM species, 3 slow-growing ***mycobacterial*** (SGM) species (two strains each), and 19 field isolates, including 18 MCC isolates (from in-use MWF) and one non-MCC isolate. . .

STP KeyWords Plus (R): LENGTH POLYMORPHISM ANALYSIS; HYPERSENSITIVITY PNEUMONITIS; ***HSP65*** GENE; FORTUITUM; ABSCESSUS; SEQUENCES; STRAINS; CRITERIA; MACHINE; ***PRIMERS***

L9 ANSWER 70 OF 71 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2003:336370 SCISEARCH <<LOGINID::20090617>>
GA The Genuine Article (R) Number: 666LZ

TI PCR-based method to differentiate the subspecies of the ***Mycobacterium*** tuberculosis complex on the basis of genomic deletions

AU Ho J L (Reprint)
CS Cornell Univ, Joan & Sanford I Weill Med Coll, Dept Med, Div Int Med & Infect Dis, Room A-421, 525 E 68th St, New York, NY 10021 USA (Reprint)
AU Huard R C; Lazzarini L C D; Butler W R; van Soolingen D
CS Cornell Univ, Joan & Sanford I Weill Med Coll, Dept Med, Div Int Med & Infect Dis, New York, NY 10021 USA; Cornell Univ, Grad Sch Med Sci, New York, NY 10021 USA; Ctr Dis Control & Prevent, Div AIDS STD & TB Lab Res, Natl Ctr Infect Dis, Atlanta, GA USA; Natl Inst Publ Hlth & Environm, NL-3720 BA Bilthoven, Netherlands
CYA USA; Netherlands

SO JOURNAL OF CLINICAL MICROBIOLOGY, (APR 2003) Vol. 41, No. 4, pp. 1637-1650.
ISSN: 0095-1137.
PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DT Article; Journal
LA English
REC Reference Count: 45
ED Entered STN: 2 May 2003
Last Updated on STN: 2 May 2003

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The classical ***Mycobacterium*** tuberculosis complex (MtbC) subspecies include ***Mycobacterium*** tuberculosis, ***Mycobacterium*** africanum (subtypes I and II), ***Mycobacterium*** bovis (along with the attenuated M. bovis bacillus Calmette-Guerin [BCG]), and ***Mycobacterium*** microti; increasingly recognized MtbC groupings include ***Mycobacterium*** bovis subsp. caprae and " ***Mycobacterium*** tuberculosis subsp. canettii" Previous investigations have documented each MtbC subspecies as a source of animal and/or human tuberculosis. However, study of these organisms is hindered by the lack of a single protocol that quickly and easily differentiates all of the MtbC groupings. Towards this end we have developed a rapid, simple, and reliable PCR-based MtbC typing method that makes use of MtbC chromosomal region-of-difference deletion loci. Here, seven ***primer*** pairs (which amplify within the loci 16S rRNA, Rv0577, IS1561', Rv1510, Rv1970, Rv3877/8, and Rv3120) were run in separate but simultaneous reactions. Each ***primer*** pair either specifically amplified a DNA fragment of a unique size or failed, depending upon the source ***mycobacterial*** DNA. The pattern of amplification products from all of the reactions, visualized by agarose gel electrophoresis, allowed immediate ***identification*** either as MtbC composed of M. tuberculosis (or M. africanum subtype II), M. africanum subtype I, M. bovis, M. bovis BCG, M. caprae, M. micron, or "M. canettii" or as a ***Mycobacterium*** other than MtbC (MOTT). This MtbC PCR typing panel provides an advanced approach to determine the subspecies of MtbC isolates and to differentiate them from clinically important MOTT species. It has proven beneficial in the management of ***Mycobacterium*** collections and may be applied for practical clinical and epidemiological use.

TI PCR-based method to differentiate the subspecies of the ***Mycobacterium*** tuberculosis complex on the basis of genomic deletions
AB The classical ***Mycobacterium*** tuberculosis complex (MtbC) subspecies include ***Mycobacterium*** tuberculosis,

Mycobacterium africanum (subtypes I and II), ***Mycobacterium*** bovis (along with the attenuated M. bovis bacillus Calmette-Guerin [BCG]), and ***Mycobacterium*** microti; increasingly recognized MtbC groupings include ***Mycobacterium*** bovis subsp. caprae and " ***Mycobacterium*** tuberculosis subsp. canettii" Previous investigations have documented each MtbC subspecies as a source of animal and/or human tuberculosis. However, study. . . a rapid, simple, and reliable PCR-based MtbC typing method that makes use of MtbC chromosomal region-of-difference deletion loci. Here, seven ***primer*** pairs (which amplify within the loci 16S rRNA, Rv0577, IS1561', Rv1510, Rv1970, Rv3877/8, and Rv3120) were run in separate but simultaneous reactions. Each ***primer*** pair either specifically amplified a DNA fragment of a unique size or failed, depending upon the source ***mycobacterial*** DNA. The pattern of amplification products from all of the reactions, visualized by agarose gel electrophoresis, allowed immediate ***identification*** either as MtbC composed of M. tuberculosis (or M. africanum subtype II), M. africanum subtype I, M. bovis, M. bovis BCG, M. caprae, M. micron, or "M. canettii" or as a ***Mycobacterium*** other than MtbC (MOTT). This MtbC PCR typing panel provides an advanced approach to determine the subspecies of MtbC isolates and to differentiate them from clinically important MOTT species. It has proven beneficial in the management of ***Mycobacterium*** collections and may be applied for practical clinical and epidemiological use.

STP KeyWords Plus (R): FRAGMENT LENGTH POLYMORPHISM; GENETIC-MARKERS; BOVIS STRAINS; WEST-AFRICA; ***HSP65*** GENE; ***IDENTIFICATION*** ; SEQUENCE; EPIDEMIOLOGY; INFECTION; ***DIAGNOSIS***

L9 ANSWER 71 OF 71 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 1999:334039 SCISEARCH <<LOGINID::20090617>>

GA The Genuine Article (R) Number: 190CL

TI Solid-phase sequence scanning for drug resistance detection in tuberculosis

AU Boyce-Jacino M T (Reprint)

CS Orchid Biocomp Inc, Alpha Ctr, Hopkins Bayview Res Campus, 5210 Eastern Ave, Baltimore, MD 21224 USA (Reprint)

AU Head S R; Parikh K; Rogers Y H; Bishai W; Goelet P

CS Orchid Biocomp Inc, Alpha Ctr, Baltimore, MD 21224 USA; Johns Hopkins Sch Hyg & Publ Hlth, Baltimore, MD USA

CYA USA

SO MOLECULAR AND CELLULAR PROBES, (APR 1999) Vol. 13, No. 2, pp. 81-87. ISSN: 0890-8508.

PB ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON NW1 7DX, ENGLAND.

DT Article; Journal

LA English

REC Reference Count: 21

ED Entered STN: 1999
Last Updated on STN: 1999

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB DNA chip arrays hold considerable promise for ***diagnostic*** sequencing of polymerase chain reaction (PCR) products. To date, however, arrays have been relatively expensive, complex to use and difficult to interpret, preventing their adaptation to the clinical lab. A moderate density array method has been developed that enables efficient, easy-to-interpret and robust solid-phase PCR product sequencing. Here, the results of ***Mycobacterium*** tuberculosis rifampin resistance

mutation detection by ***primer*** -extension-based sequence scanning of the rpoB gene of M. tuberculosis are presented. Rifampin resistant clinical isolates were ***identified*** in as little as 1 h post PCR amplification with visual results detection. (C) 1999 Academic Press.

AB DNA chip arrays hold considerable promise for ***diagnostic*** sequencing of polymerase chain reaction (PCR) products. To date, however, arrays have been relatively expensive, complex to use and difficult. . . density array method has been developed that enables efficient, easy-to-interpret and robust solid-phase PCR product sequencing. Here, the results of ***Mycobacterium*** tuberculosis rifampin resistance mutation detection by ***primer*** -extension-based sequence scanning of the rpoB gene of M. tuberculosis are presented. Rifampin resistant clinical isolates were ***identified*** in as little as 1 h post PCR amplification with visual results detection. (C) 1999 Academic Press.

ST Author Keywords: ***Mycobacterium*** tuberculosis; drug resistance; DNA arrays; GBA; solid-phase; ***primer*** extension

STP KeyWords Plus (R): HEAT-SHOCK-PROTEIN; CATALASE-PEROXIDASE GENE; ***MYCOBACTERIUM*** -TUBERCULOSIS; SUBSPECIFIC DIFFERENTIATION; ISONIAZID RESISTANCE; BIT ANALYSIS; ***HSP65*** ; ***IDENTIFICATION*** ; SENSITIVITY; ETHAMBUTOL